

Fri Nov 7 08:48:20 2003

us-10-081-817a-19-plus-1-12-of-seq3.rge

Page 1

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 10:03:01 ; Search time 1999 Seconds  
(without alignments)  
11521.821 Million cell updates/sec

Title: US-10-081-817a-19-PLUS-1-12-OF-SEQ3  
Sequence: 1 CGGCGG999G9GCGGCGG9.....CCGCGCGCATGAGCTCGCC 563

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl :  
1: gb\_ba :  
2: gb\_hg :  
3: gb\_in :  
4: gb\_om :  
5: gb\_ov :  
6: gb\_pac :  
7: gb\_ph :  
8: gb\_pl :  
9: gb\_pr :  
10: gb\_ro :  
11: gb\_sts :  
12: gb\_sy :  
13: gb\_un :  
14: gb\_vi :  
15: em\_ba :  
16: em\_fun :  
17: em\_hum :  
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19: em\_mu :  
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24: em\_ph :  
25: em\_pl :  
26: em\_ro :  
27: em\_sts :  
28: em\_un :  
29: em\_vi :  
30: em\_hg\_hum :  
31: em\_hg\_inv :  
32: em\_hg\_other :  
33: em\_hg\_mus :  
34: em\_hg\_pin :  
35: em\_hg\_rtd :  
36: em\_hg\_mam :  
37: em\_hg\_vit :  
38: em\_sy :  
39: em\_hggo\_hum :  
40: em\_hggo\_mus :  
41: em\_hggo\_other :

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
C 1	500.5	88.9 127488	2 AC022095	AC022095 Homo sapi
C 2	498	88.5 168347	2 AC025336	AC025336 Homo sapi
C 3	487	88.5 190024	2 AC122714	AC122714 Homo sapi
C 4	481.8	85.6 166777	2 AC106813	AC106813 Homo sapi
C 5	481.8	85.6 130129	2 AC106803	AC106803 Homo sapi
C 6	481.8	85.6 130129	2 AC106803	AC106803 Homo sapi
C 7	129	22.9 190	6 BD082141	BD082141 Reagents
C 8	129	22.9 190	6 BD082137	BD082137 Reagents
C 9	90	18.0 570	6 AR252648	AR252648 Sequence
C 10	90	18.0 570	6 AX201348	AX201348 Sequence
C 11	90	18.0 570	6 AX403520	AX403520 Sequence
C 12	89	15.8 244	6 BD082138	BD082138 Reagents
C 13	74	13.6 125020	2 AF429315	AF429315 Homo sapi
C 14	71	12.6 172550	2 AP005772	AP005772 Oryza sat
C 15	68.2	12.1 215852	2 AC084804	AC084804 Mus muscu
C 16	66.8	11.9 215852	2 AC022663	AC022663 Homo sapi
C 17	64.4	11.5 63082	2 PM12H12B	PM12H12B Macaca mu
C 18	64.4	11.4 1007	11 PM3H11G	PM3H11G Macaca mu
C 19	63.2	11.2 167624	2 AC143286	AC143286 Macaca mu
C 20	63.2	11.0 1082	11 AC022663	AC022663 Homo sapi
C 21	62.2	11.0 63082	2 AC139773	AC139773 Homo sapi
C 22	62.2	11.0 63082	2 AC139773	AC139773 Homo sapi
C 23	62	11.0 63082	2 AC139773	AC139773 Homo sapi
C 24	61.8	11.0 72645	2 AC112672	AC112672 Mus muscu
C 25	61.8	11.0 101509	2 AC027353	AC027353 Homo sapi
C 26	61.8	11.0 187413	2 AC141871	AC141871 Mus muscu
C 27	61.6	10.9 1965	10 AF411253	AF411253 Mus muscu
C 28	61.6	10.9 125020	9 AF429315	AF429315 Homo sapi
C 29	61.6	10.9 125020	9 AC091093	AC091093 Papio anu
C 30	61.6	10.9 167077	2 AC091093	AC091093 Papio anu
C 31	61.6	10.8 2685	6 H0MBA8A10	H0MBA8A10 Sequence
C 32	61	10.8 43058	6 AX333047	AX333047 Sequence
C 33	61	10.8 43058	6 AX333047	AX333047 Sequence
C 34	61	10.8 43058	6 AX411306	AX411306 Sequence
C 35	61	10.8 43058	9 AE006462	AE006462 Homo sapi
C 36	60.8	10.8 258002	2 AC141419	AC141419 Pan trogl
C 37	60.8	10.7 159980	2 AF005743	AF005743 Oryza sat
C 38	59.6	10.6 1065	11 PM2B12B	PM2B12B Sequence
C 39	59.6	10.6 1065	11 PM2B12B	PM2B12B Sequence
C 40	59.6	10.6 1065	11 PM2B12B	PM2B12B Sequence
C 41	58.8	10.4 85268	2 AC022648	AC022648 Homo sapi
C 42	58.8	10.4 85268	2 AC022648	AC022648 Homo sapi
C 43	58.8	10.4 85434	2 AC066610	AC066610 Homo sapi
C 44	58.8	10.4 85434	2 AC066610	AC066610 Homo sapi
C 45	58.8	10.4 224777	2 AC138109	AC138109 Mus muscu

ALIGNMENTS

RESULT 1  
AC022095/c 127488 bp DNA linear HTG 20-APR-2001  
LOCUS Homo sapiens chromosome 5 clone CTB-3688, WORKING DRAFT SEQUENCE,  
DEFINITION 13 unordered pieces.  
ACCESSION AC022095  
VERSION AC022095.5 GI:13699618  
KEYWORDS HTG: HTGS PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukariyotia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 DOE Joint Genome Institute.  
TITLE Sequencing of Human Chromosome 5

JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 127488)  
 AUTHORS DOE Joint Genome Institute.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 COMMENT On Apr 20, 2001 this sequence version replaced gi:7711676.  
 -----Genome Center  
 Center: Joint Genome Institute  
 Center Code: JGI  
 Web site: <http://www.jgi.doe.gov>

Project Information  
 Project Name: 78060  
 Center Name: C17978SKB\_3688

Summary Statistics  
 Consensus quality: 110477 bases at least Q40  
 Consensus quality: 117221 bases at least Q30  
 Consensus quality: 120225 bases at least Q20  
 Estimated insert size: 131000; pulse field gel estimation  
 Estimated insert size: 126288; sum-of-coverage estimation  
 Quality coverage: 7.48 in Q20 bases; pulse field gel estimation  
 Quality coverage: 7.76 in Q20 bases; sum-of-coverage estimation.  
 NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1116: contig of 1116 bp in length  
 1117 1216: gap of unknown length  
 1217 1254: contig of 1038 bp in length  
 2255 2354: gap of unknown length  
 2355 3412: contig of 1058 bp in length  
 3413 5005: contig of 1493 bp in length  
 5006 5105: gap of unknown length  
 5106 7647: contig of 2542 bp in length  
 7648 10237: contig of 2490 bp in length  
 10238 10337: gap of unknown length  
 10338 12440: contig of 2103 bp in length  
 12441 12540: gap of unknown length  
 12541 15935: contig of 3395 bp in length  
 15936 16036: gap of unknown length  
 16036 24396: contig of 8361 bp in length  
 24397 24496: gap of unknown length  
 24497 39085: contig of 14589 bp in length  
 39086 39185: gap of unknown length  
 39186 60545: contig of 21360 bp in length  
 60546 60645: gap of unknown length  
 60646 79490: contig of 18845 bp in length  
 79491 79590: gap of unknown length  
 79591 127488: contig of 47898 bp in length.

## FEATURES

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 /mol\_type="Genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="5"  
 /clone="C1B-3688"  
 /clone\_lib="CalTech human BAC library B"  
 BASE COUNT 31643 a 32392 c 31616 g 30626 t 1211 others

Query Match 88.9%; Score 500.6; DB 2; Length 127488;  
 Best Local Similarity 95.9%; Pred. NO. 2.2e-74;  
 Matches 541; Conservative 0; Mismatches 5; Indels 18; Gaps 2;

1 CGCGCGGAGGCGCGCGGAGTGAAGCTGATGCTCCCTGCGCCCTCCACCTCCCGAGG 60

|||||  
 Db 84291 CGCGCGGAGGAGGCGCGGAGTGAAGCTGATGCTCCCTGCGCCCTCCACCTCCCGAGG 84232  
 Qy 61 CGCAGAGGCGCGCCACGAGGACCCCACTGAGCCGACGTTGCTGAGTCAAGAG 120  
 Db 84231 CGCAGAGGCGCGCCACGAGGACCCCACTGAGCCGACGTTGCTGAGTCAAGAG 84172  
 Qy 121 CAGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
 Db 84171 CAGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 84112  
 Qy 181 CCTTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
 Db 84111 CCTTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
 Qy 241 AGACCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
 Db 84068 AGACCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 84009  
 Qy 301 CT-CTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 359  
 Db 84008 CTCTCTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 83949  
 Qy 360 GGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 419  
 Db 83948 GGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 83889  
 Qy 420 GAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 479  
 Db 83888 GAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 83829  
 Qy 480 ACCGGGTATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 539  
 Db 83828 ACCGGGTATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 83769  
 Qy 540 AGCG 563  
 Db 83768 AGCG 83745

## RESULT 2

AC025336/c

LOCUS

DEFINITION

Homo sapiens chromosome 5 clone RP11-451H23 map 5, WORKING DRAFT

AC025336

VERSION

AC025336.2 GI:7328761

KEYWORDS

HMG PHASE1; HMG\_DRAFT.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

Unpublished

2 (bases 1 to 168347)

Britten, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Anderson, S., Baldwin, J., Barna, N., Basile, V., Bedalov, G.,

Boguski, L., Boulikas, A., Brown, A., Bunker, G.,

Campione, A., Casale, P., Cawthon, C., Cheng, Y., Collins, S.,

Coryell, W., D'Onofrio, P., DeRubeis, R., Dewar, K., Diaz, J.S.,

Dodge, S., Domino, M., Doyle, M., Ferris, P., Fitzhugh, W., Gage, D.,

Galligan, J., Gargano, S., Gildea, S., Gish, W., Gish, W., Graham, L.,

Grand-Pierre, N., Grant, G., Hager, B., Hager, B., Heald, A., Horton, L.,

Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karas, A.,

Klein, J., Lacombe, K., Lamazares, R., Landers, T., Lebeck, J.,

Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N.,  
 McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPherson, R.,  
 Meltzer, J., Menus, L., Mihov, T., Miranda, C., Miska, V., Morrow, J.,  
 Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
 O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,  
 Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,

TITLE  
JOURNAL

## COMMENT

Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, R., Stojanovic, N., Subramanian, A., Talmac, J., Testa, S., Theodore, J., Tirrell, A., Travers, M., Trigglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wymann, D., Ye, W., Young, G., Zannon, J., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted 108-MAR-2000 Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 25, 2000 this sequence version replaced g1:7210017.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WITB  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 Project information

Center project name: 451 H 23  
 Sequencing Summary Statistics  
 Sequencing Vector: M13; M77815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 150422 bases at least Q40  
 Consensus quality: 159524 bases at least Q30  
 Consensus quality: 163013 bases at least Q20  
 Insert size: 165247; sum-of-contigs  
 Quality coverage: 3.6 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 32 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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FEATURES  
source

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 Matches 540; Conservative 0; Mismatches 5; Indels 19; Gaps 2;

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QY 61 CGCGAGAGGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 145142 CGCGAGAGGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 145083
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DB 145022 C-----CCTCACACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 144981
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DB 144980 AGACCCGAAAGCGAAGAGTGGGAGCGGAGTGGAGCTCGCGAGAGAGAGAGAG 144921
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 DEFINITION Homo sapiens chromosome 5, clone RP11-451H23, complete sequence.

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
REFERENCE 2 (bases 1 to 190024)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Direct Submission
REFERENCE 3 (bases 1 to 190024)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Submitted (04-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
JOURNAL Drive, Walnut Creek, CA 94598, USA
COMMENT On Mar 4, 2003 this sequence version replaced gi:21206277.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.9.
NOTE: Shatter libraries failed to verify the dinucleotide repeat
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124370-125308. Forced join 124996.
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Query Match 88.5%; Score 498; DB 9; Length 190024;
Best Local Similarity 95.7%; Pred. No. 5,3e-74;
Matches 540; Conservative 0; Mismatches 5; Indels 19; Gaps 2;

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DB 81411 CGGAGAGAGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 81352
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DB 81249 AGACCCGAAAGCGAAGAGTGGGAGCGGAGTGGAGCTTCGCGAGAGAGAGAGAG 81190
QY 301 CT-CTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 359
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Fri Nov 7 08:48:20 2003

us-10-081-817a-19-plus-1-12-of-seq3.rge

Page 5

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SOURCE	Homo sapiens		
ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 166777)		
AUTHORS	DOE Joint Genome Institute.		
TITLE	Sequencing of Human Chromosome 5		
JOURNAL	2 (bases 1 to 166777)		
REFERENCE	DOE Joint Genome Institute.		
AUTHORS	Direct Submission		
TITLE	Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint		
JOURNAL	Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		
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AUTHORS	Direct Submission		
TITLE	Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint		
JOURNAL	Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		
	On Mar 7, 2002 this sequence version replaced gi:18369924.		
COMMENT	-----Genome Center		
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	Center Code: JGI		
	Web site: http://www.jgi.doe.gov		
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	Project Information		
	Center Project Name: 1519801		
	Center clone name: RPCI-11_586L9		
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	Summary Statistics		
	163497 bases at least Q40		
	Consensus quality: 166071 bases at least Q30		
	Consensus quality: 166432 bases at least Q20		
	Estimated insert size: 186250; agarose-fp estimation		
	Estimated insert size: 166577; sum-of-contigs estimation		
	Estimated insert size: 10.51 in Q20 bases; agarose-fp estimation		
	Quality coverage: 10.51 in Q20 bases; sum-of-contigs estimation		
	Quality coverage: 10.51 in Q20 bases; sum-of-contigs estimation		
	NOTE: This is a working draft sequence. It currently		
	consists of 3 contigs. Gaps between the contigs		
	are represented as runs of 'N'. The order of the pieces		
	is believed to be correct as given, however the sizes		
	of the gaps between them are based on estimates that have		
	been provided by the submitter.		
	This sequence will be replaced		
	by the finished sequence as soon as it is available and		
	the accession number will be preserved.		
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119566	GACCGGATTAAGAGAGCTCGTGGCTTTGCGCGGCGAGCGCGAGAGTTCCCGCGCGCGCC 119625							
539	GAGCGCGCGCGCGCGCATGAGACTCGCC 563							
119626	GAGCGCGCGCGCGCGCATGAGACTCGCC 119650							
RESULT 5								
AC108083/c								
LOCUS	130129 bp DNA linear HTG 25-JAN-2002							
DEFINITION	Homo sapiens chromosome 5 clone CTD-2013L15, WORKING DRAFT							
SEQUENCE	4 unordered pieces.							
AC108083								
AC108083.1	GI:18369929							
VERSION	HTG: HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEPIN.							
KEYWORDS	Homo sapiens (human)							
SOURCE	Homo sapiens							
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
REFERENCE	1 (bases 1 to 130129)							
AUTHORS	DOE Joint Genome Institute.							
TITLE	Sequencing of Human Chromosome 5							

JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 130129)
AUTHORS	DOE Joint Genome Institute.
TITLE	Direct Submission
JOURNAL	Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598. USA
COMMENT	-----Genome Center

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Project Information
Center Project Name: 632820
Center clone name: CITB-H1_2013L15
-----

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Summary Statistics
Consensus quality: 124488 bases at least Q40
Consensus quality: 128031 bases at least Q30
Consensus quality: 128842 bases at least Q20
Estimated insert size: 135000; agarose-fp estimation
Estimated coverage: 7.66 in Q20 bases; agarose-fp estimation
Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation
NOTE: This is a "working draft" sequence. It currently
consists of 4 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

```

FEATURES			
*	4320:	contig of 4320 bp in length	
1	4420:	gap of unknown length	
*	4421:	gap of unknown length	
*	4422:	contig of 19222 bp in length	
*	23713:	gap of unknown length	
*	23812:	gap of unknown length	
*	23813:	contig of 24790 bp in length	
*	48602:	gap of unknown length	
*	48603:	gap of unknown length	
*	48703:	contig of 81427 bp in length	
	130129:	contig of 81427 bp in length	
	Location/Qualifiers		

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/organism="Homo sapiens"
/mol_type="Genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2013A5"
/clone_1fb="CalTech human BAC library D"
BASE COUNT      35337 a      33397 c      30949 g      31146 t      300 other
ORIGIN

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	Query Match	Best Local Similarity	85.6%	Score 481.8	DB 2	Length 130129
	Matches 526	Conservative 0	Mismatches 71	Indels 20	Gaps 3	
QY	1	CGGCGGAGAGCGCGCGCGGAGTGAAGCCTGATCGTCCCTGAGCCCTCCACACTGCCAGG				60
Db	24569	CGGCGGAGAGCGCGCGCGGAGTGAAGCCTGATGCTCCTGGCCCTCCACCTCCCAAG				24511
QY	61	CGCAAAAGGCGCCCAAGAAACCCCACTGCGCAGCTTGCAAGCTGTGGATTCAGAG				120
Db	24509	CGCAAAAGGCGCCCAAGAAACCCCACTGCGCAGCTTGCAAGCTGTGGATTCAGAG				24455
QY	121	CAGGAGCCAGGAGACCGAAGTATCGCGCGCGCGCCCTGCGCTGTGCGAGGAAGCT				180
Db	24449	CAGGAGCCAGGAGACCGAAGTATCGCGCGCGCGCCCTGCGCTGTGCGAGGAAGCT				24390
QY	181	CCTTCACGAGGAGAACTCCCTCCACCCGAGCCCAAGCCTGTGCGAGGGGCGCGTGGGCTC				240
Db	24389	CCTTCACCGAGGAGAACTCCCTCCACCCGAGCCCAAGCCTGTGCGAGGGGCGCGTGGGCTC				24348
QY	241	AGACCCGAAAGCAAGAGTGTGCGGCGCGAGGCTGGGCTCTCGCGAGACAAAGGCGGAGCTGC				300
Db	24347	AGACCCGAAAGCAAGAGTGTGCGGCGCGAGGCTGGGCTCTCGCGAGACAAAGGCGGAGCTGC				24288

QY	302	CT-CTCTCAAGAGGCCCAAGCGCTCTCCAAAGAGAAAGTCTCTGAGAGCCCGGGGCAAGG	359
Db	24287	CTGCTCTCAAGAGGCGCCCAAGCGCTCTCCAAAGAGAAAGTCTCTGAGAGCCCGGGGCAAGG	24228
QY	360	GGGGGACGGGCTTCCCAAGGCGCCGCGAGCAGAGATTGAGCCAGGSCACGGCGCT	419
Db	24227	GGGGGACGGGCTTCCCAAGGCGCCGCGAGCAGAGATTGAGCCAGGSCACGGCGCT	24188
QY	420	GAGCGSAGCCGGCAGGGCTTTCTCAAGACCGCGGCGCAGGCGCGCTGAGAGGGGCGAG	479
Db	24167	GAGCGSAGCCGGCAGGGCTTTCTCAAGACCGGGGCGCAGGCGCGCTGAGAGGGGCGAG	24108
QY	480	ACGGGATTAAGAAAGCTCTGTGCTTACCGGAGCAGCCGACAGATTCCCGCGCGCCCG	539
Db	24107	ACGGGATTAAGAAAGCTCTGTGCTTACCGGAGCAGCCGACAGATTCCCGCGCGCCCG	24048
QY	540	AGCCCCCGGCGCTAAGGCTTGGC	562
Db	24047	AG-CCCCGGCGCTAAGGCTTGGC	24026

RESULT 6  
 BD082141  
 LOCUS  
 ACCESION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Zea mays  
 Zea mays  
 Zea mays  
 GI:22627751  
 1  
 22225-A/5.  
 562 bp  
 DNA  
 linear  
 PAT 27-AUG-2002  
 Regents and methods useful for detecting diseases of the lung.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	Clade; Panticoideae; Andropogoneae; Zea.			
1	(Pages 1 to 562)			
	Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Grados, E.N., Hodges, S.C., Klats, M.R., Kratochvil, J.D., Rapp, L.R., Russell, J.C. and Stroupe, S.D.			
	Patients and methods useful for detecting diseases of the lung			
	ABSTRACT LABORATORY 513225-A 5 13-NOV-2001;			
	PN JP 2001562325, 5/5			

```

PI      N FRIEDMAN,
PI      JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI
KLASS,
PI      JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D
PI      STROBE
PC      C12N5/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC
Srandness: Single;
CC      Topology: Linear;
PI      Key      Location/Qualifiers.
FEATURES
Source      1..562

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[illegible]

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Db      61 GAAGCCTGCGCTTGGCCCGGAGCCGAGGTTCCCGCGCGCCCGGAGCCCGCGCG 120
QY      551 CATGAGCTCGCC 563
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Db      121 CATGAGCTCGCC 133

RESULT 7
BD082137 190 bp DNA linear PAT 27-AUG-2002
LOCUS     Reagents and methods useful for detecting diseases of the lung.
DEFINITION
ACCESSION BD082137.1 GI:22627747
VERSION    JP 2001522225-A/1.
KEYWORDS   Zea mays
SOURCE      Zea mays
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 190)
            Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,
            Granados,E.N., Hodges,S.C., Klaas,M.R., Kratochvil,J.D., Rapp,L.R.,
            Russell,J.C. and Stroupe,S.D.
            Reagents and methods useful for detecting diseases of the lung
            Patent: JP 2001522225-A 1 13-NOV-2001;
            ABBOTT LABORATORIES
            PN JP 2001522225-A/1
COMMENT    PD 13-NOV-2001
            PF 30-JAN-1998 JP 1998533078
            PR 30-JAN-1997 US 08/791710
            PI PATRICIA A BILHNG MEDEL,MAURICE COHEN,TRACEY L COLPITTS,PAULA
            PI N FRIEDMAN,
            PI JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES,MICHAEL R PI
            PI KLAAS,
            PI JON D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C RUSSELL,STEPHEN D
            PI STROUPE
            PC C12N15/63,C12N5/10,C12Q1/68,C07K14/47//C07K16/30,G01N33/574 CC
            Strandedness: Single;
            CC Topology: Linear;
            FH Key Location/Qualifiers.
            1..190
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /db_xref="taxon:4577"

BASE COUNT 18 a 69 c 67 g 32 t 4 others

ORIGIN
Query Match 22.9%; Score 129; DB 6; Length 190;
Best Local Similarity 97.0%; Pred. No. 6,9e-12;
Matches 129; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      431 GCAGGCGCTTTCAGAGCGCGGCGAGCGCGGCTGAGGGGCGAGGACCGGGTATTA 490
        |||||||
Db      1 GCAGGCGCTTTCAGAGCGCGGCGAGCGCGGCTGAGGGGCGAGGACCGGGTATTA 60
        |||||||
QY      491 GAAGCCTGCGCTTGGCCCGGAGCCGAGGTTCCCGCGCGCCCGGAGCCCGCGCG 550
        |||||||
Db      61 GAGGCGCTTTCAGAGCGCGGCGAGCGCGGCTGAGGGGCGAGGACCGGGTATTA 120
        |||||||
QY      551 CATGAGCTCGCC 563
        |||||||
Db      121 CATGAGCTCGCC 133

RESULT 8
BD082142 519 bp DNA linear PAT 27-AUG-2002
LOCUS     Reagents and methods useful for detecting diseases of the lung.
DEFINITION
ACCESSION BD082142.1 GI:22627752
VERSION    JP 2001522225-A/6.
KEYWORDS

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SOURCE      Zea mays
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 519)
            Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,
            Granados,E.N., Hodges,S.C., Klaas,M.R., Kratochvil,J.D., Rapp,L.R.,
            Russell,J.C. and Stroupe,S.D.
            Reagents and methods useful for detecting diseases of the lung
            Patent: JP 2001522225-A 6 13-NOV-2001;
            ABBOTT LABORATORIES
            PN JP 2001522225-A/6
COMMENT    PD 13-NOV-2001
            PF 30-JAN-1998 JP 1998533078
            PR 30-JAN-1997 US 08/791710
            PI PATRICIA A BILHNG MEDEL,MAURICE COHEN,TRACEY L COLPITTS,PAULA
            PI N FRIEDMAN,
            PI JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES,MICHAEL R PI
            PI KLAAS,
            PI JON D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C RUSSELL,STEPHEN D
            PI STROUPE
            PC C12N15/63,C12N5/10,C12Q1/68,C07K14/47//C07K16/30,G01N33/574 CC
            Strandedness: Single;
            CC Topology: Linear;
            FH Key Location/Qualifiers.
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BASE COUNT 78 a 190 c 170 g 81 t

ORIGIN
Query Match 16.0%; Score 90; DB 6; Length 519;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      474 GCGAGACCGGGTATGAGAGCGCTCGGCGCGGAGCGGAGGTTCCCGCGCG 533
        |||||||
Db      1 GCGAGACCGGGTATGAGAGCGCTCGGCGCGGAGCGGAGGTTCCCGCGCG 60
        |||||||
QY      534 GCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 563
        |||||||
Db      61 GCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 90
        |||||||

RESULT 9
AX201348 569 bp DNA linear PAT 30-AUG-2001
LOCUS     Sequence 27 from Patent WO0153486.
DEFINITION
ACCESSION AX201348
VERSION    AX201348.1 GI:15391167
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1
            Aabkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,
            Stone,D.M., Watanabe,C.K. and Wood,W.I.
            Compositions and methods for the treatment of tumour
            Patent: WO 0153486-A 27 26-JUL-2001;
            Genentech, Inc. (US)
            Location/Qualifiers
            1..569
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

BASE COUNT 128 a 190 c 170 g 81 t

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Query Match
Best Local Similarity 16.0%; Score 90; DB 6; Length 569;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGATATAAGAGCTGTGCTTGGCCCGGAGCGGAGGTTCCCGCGC 533
DB 1 GCGAGGACCGGGATATAAGAGCTGTGCTTGGCCCGGAGCGGAGGTTCCCGCGC 60
QY 534 GCGCCGAGCCCGCGCCCATGAAGCTCGCC 563
DB 61 GCGCCGAGCCCGCGCCCATGAAGCTCGCC 90

RESULT 10
AR252648
LOCUS AR252648
DEFINITION Sequence 407 from patent US 6478825.
ACCESSION AR252648
VERSION AR252648.1 GI:27300556
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT
ORIGIN
129 a 190 c 170 g 81 t

Query Match
Best Local Similarity 16.0%; Score 90; DB 6; Length 570;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGATATAAGAGCTGTGCTTGGCCCGGAGCGGAGGTTCCCGCGC 533
DB 1 GCGAGGACCGGGATATAAGAGCTGTGCTTGGCCCGGAGCGGAGGTTCCCGCGC 60
QY 534 GCGCCGAGCCCGCGCCCATGAAGCTCGCC 563
DB 61 GCGCCGAGCCCGCGCCCATGAAGCTCGCC 90

RESULT 11
AX403520
LOCUS AX403520
DEFINITION Sequence 407 from Patent WO0073454.
ACCESSION AX403520
VERSION AX403520.1 GI:21437002
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT
ORIGIN
129 a 190 c 170 g 81 t

Query Match
Best Local Similarity 16.0%; Score 90; DB 6; Length 570;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGATATAAGAGCTGTGCTTGGCCCGGAGCGGAGGTTCCCGCGC 533
DB 1 GCGAGGACCGGGATATAAGAGCTGTGCTTGGCCCGGAGCGGAGGTTCCCGCGC 60
QY 534 GCGCCGAGCCCGCGCCCATGAAGCTCGCC 563
DB 61 GCGCCGAGCCCGCGCCCATGAAGCTCGCC 90

RESULT 12
BD082138
LOCUS BD082138
DEFINITION Reagents and methods useful for detecting diseases of the lung.
ACCESSION BD082138
VERSION BD082138.1 GI:22627748
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
P.N. Friedman, Julian Gordon, Edward N. Grandos, Steven C. Hodges, Michael R. Pi, Jon D. Kratochvil, Lisa Roberts Rapp, John C. Russell, Stephen D. Russell, J.C. and Strope, S.D.
Reagents and methods useful for detecting diseases of the lung
Patent: JP 2001522225-A 2 13-NOV-2001,
ABBOTT LABORATORIES
PN JP 2001522225-A/2
PD 13-NOV-2001 JP 1998533078
PF 30-JAN-1998 JP 1998533078
PR 31-JAN-1997 US 08/791710
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULIA N FRIEDMAN, JULIAN GORDON, EDWARD N GRANDOS, STEVEN C HODGES, MICHAEL R PI, JULIAN KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D STROPE, JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D RUSSELL, J.C. and Strope, S.D.
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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/organism="Zea mays"
/mol_type="genomic DNA"
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BASE COUNT
ORIGIN
25 a 97 c 82 g 39 t 1 others

Query Match
Best Local Similarity 15.8%; Score 89; DB 6; Length 244;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGATATAAGAGCTGTGCTTGGCCCGGAGCGGAGGTTCCCGCGC 533
DB 1 GCGAGGACCGGGATATAAGAGCTGTGCTTGGCCCGGAGCGGAGGTTCCCGCGC 60
QY 534 GCGCCGAGCCCGCGCCCATGAAGCTCGCC 563
DB 61 GCGCCGAGCCCGCGCCCATGAAGCTCGCC 90

RESULT 13

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AF429315/c 125020 bp DNA linear PRI 18-JAN-2002

LOCUS AF429315

DEFINITION Homo sapiens junctophilin 3 (JPH3) gene, partial cds.

ACCESSION AF429315

VERSION AF429315.1 GI:17646244

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

Homosapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S.,  
Ingberoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A.,  
Potter,N.T., Ross,C.A. and Margolis,R.L.  
A repeat expansion in the gene encoding junctophilin-3 is  
associated with Huntington disease-like 2

TITLE Nat Genet. 29 (4), 377-378 (2001)

JOURNAL

MEDLINE 21383737

PUBMED 11694876

REFERENCE 2 (bases 1 to 125020)

AUTHORS Holmes,S.E., Ingberoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L.  
Direct Submision (05-OCT-2001) Psychiatry, Johns Hopkins Medical  
Submitted (05-OCT-2001) Baltimore, MD 21287, USA  
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA

TITLE Location/Qualifiers

JOURNAL

FEATURES

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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="16"  
/map=16q24.3; between D16S520 and WI-12410"  
/note="Isolated from a patient with Huntington's  
Disease-Like 2 (HDL2)"  
complement(35581..35746)  
/rpt\_type=tandem  
/rpt\_unit=ctg  
complement(<36507..>36887)  
/gene="JPH3"  
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/product="junctophilin 3"  
complement(<36507..>36887)  
/gene="JPH3"  
/note="component of the functional complex between plasma  
membrane and endoplasmic reticulum"

CDS

gene

mRNA

repeat\_region

BASE COUNT 29056 a 32731 c 30696 g 28283 t 4254 others

ORIGIN

Query Match 13.1%; Score 74; DB 9; Length 125020;

Best Local Similarity 13.2%; Pred. No. 0.0014; Indels 1; Gaps 1;

Matches 64; Conservative 224; Mismatches 197;

DY 45 CCRCCACCCTCCAGGCGCAGAAGGCCGCCAGAGAGACCCCAGTGCCTCCGACGTTGCCAC 104

DY 17694 SGTISYSYSCCKWMSWGSCYKCMKKYISGMSSYSTSMGYSSISPSCKRYKRSWSMKTKTS 17635

DY 105 GGRCTGGGAATCAGAGCAGAGGAGCAGAGGAGCAGAGAACTGCGCGCCCCCGCCCTTGCCC 164

DY 17634 KSYRRKRKYIYYGGGKRAKKYICAGRRRMSYWKCCAKWMMSYCCWSYCMTYYSKST 17575

DY 165 TGGCGCGAAGAACGTCCTCACACNAGAGGAACCTCCCTCCACCGCCGACGCTCGAC 224

DY 17574 YKSSTCYKRGYVWGSKITCYSAAGSKRSMTYICMMRSKSSSMSMARSSMCWGWAGVR 17515

DY 225 GGGGCGCGTGGGTCAAGCCGCAAGGCGGGCGGGGTGGGCTTCGCGAGA 284

Accession	Version	Keywords	Organism	Reference	Journal	Comment	Features	Base Count	Origin	Query Match	Best Local Similarity
17514				RSKRSRGMGACWGRSSKGRBRTSGMKRA							
285				CAAAGCGCGGCTCCTCTCTCAGAGAGG							
17454				CYCMWRTYRTKRTSNQWYMKMSWYKRYK							
345				GCCCCGGGCGAGGAGGCGGACACGGCCT							
17394				SSYSTSCWKS CMWYSMMKCMKMTSFKK							
404				GCCAGGACACCGCGCTGACCGGACGCGG							
17334				RSKCYSTKSYKKRGKMKMGWGMKRSKWS							
464				CGCTGAGGGGCGGAGGACCGGCTATAGA							
17274				GRSTKSKKSSMRMASSKCTYSSWSNNR							
524				TTCCCC 529							
17214				TTCCCC 17209							
AP005772				AP005772							
LOCUS				LOCUS							
DEFINITION				DEFINITION							
ACCESSION				ACCESSION							
VERSION				VERSION							
KEYWORDS				KEYWORDS							
SOURCE				SOURCE							
ORGANISM				ORGANISM							
REFERENCE				REFERENCE							
AUTHORS				AUTHORS							
JOURNAL				JOURNAL							
TITLE				TITLE							
REFERENCE				REFERENCE							
JOURNAL				JOURNAL							
COMMENT				COMMENT							
FEATURES				FEATURES							
source				source							
BASE COUNT				BASE COUNT							
Origin				Origin							
Query Match				Query Match							
Best Local Similarity				Best Local Similarity							

Matches	222;	Conservative	0;	Mismatches	295;	Indels	6.	Gaps	1.
---------	------	--------------	----	------------	------	--------	----	------	----

Oy 34 CGTCCCTGGAGCGCTCTCACTCCCGCAGGCAGACGCCACGAGAGACCCCGAGTGGC 93  
 Db 91602 CGACCTTACCGGGCGCAACTGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 91542  
 Oy 94 GACGTTGCCACGCTCTGGGATCAGAGGCAGAGGACCCAGAACTCGCCCGCCC 153  
 Db 91542 NNNNNNNNNNNNGGCGCGCGCGCGCGGNNCGNCGCGNCGGGCCCGCGCCCGGGGC 91483  
 Oy 154 CGCCCTCGCCCTCGCGCGAGAGAACTCTCACGAGAGAACTCTCTCACTCCGCGCC 213  
 Db 91482 CCGGCGCGGCGAGTCTGCGCGCGCGCGCGCGNCGGGGGGCGGGGACCGCGNCCCCCGCGCG 91423  
 Oy 214 CAGCCCTCAGAGGGGGCGCGTGGGTCAAGCCGAAACGAAAGTGGGCGCGGGTGGG 273  
 Db 91422 GNNGGCGGGGCGCCCGCGGGGCGGGGCGCGCGNCGCGCGNCGCGCCCGCGGGG 91363  
 Oy 274 CCTCGCGGAGACAAAGCGCGGGGCTGCTCTCTTCAAGGGCCCGACGCGCTTCCAAAGG 333  
 Db 91362 GCGCGCGGCGGG 91303  
 Oy 334 AAGTCTC----GAGGCTCCGCGCAGGAAAGGGGCACGGCTTCCAGGCGCGCGCG 387  
 Db 91302 GCGGCGCGCGGGGGGCG 91243  
 Oy 388 CCGCAGCAGAGAACTTGGGCGAGGGCAGCGCGCTGAGCGGAGCGGGCAGGGCTTCTCAGGA 447  
 Db 91242 CGGGGCGCGGGGGGCGCGCGCGCGCGCGCGCGGGGGGGCGGGGGGGCGCGCGCGGGC 91183  
 Oy 448 GCGCGGCGCGAGCGCGCGCGCTTGAAGGGGCGAGGACCGGATATGAAGGCTTGTGGACCTTG 507  
 Db 91182 CCGGGGGGCGCGCGCGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 91123  
 Oy 508 CCGGGGAGCGCGCAGGTTCCCGCGCGCGCCCGAGCCCGCGCGC 550  
 Db 91122 CGGGGCGCGNCCGGGGCGCGGGGGGGGGGGCGCGCGCGCGCGCGC 91080

[illegible]



```

XX PT Diagnosing and/or determining a predisposition to a cellular
XX PT proliferative disorder of breast tissue, in particular breast cancer,
XX PT by determining the state of methylation of one or more nucleic acids
XX PT isolated from the subject
XX
XX Disclousure; Fig 9A; 115pp; English.
XX
XX CC The present invention relates to a method of diagnosing a cellular
XX CC proliferative disorder of breast tissue, which involves determining the
XX CC state of methylation of one or more nucleic acids isolated from the
XX CC subject, where the state of methylation of the nucleic acids as compared
XX CC with a state of methylation from a subject not having the cellular
XX CC proliferative disorder of breast tissue is indicative of a cellular
XX CC proliferative disorder of breast tissue in the subject. The nucleic acids
XX CC may be TWIST, HOMA5, NES-1, retinoic acid receptor beta (RARbeta),
XX CC oestrogen receptor, cyclin D2, Wilms' tumour gene (WT-1), 14.3.3 sigma,
XX CC HIN-1 or RASSF1A. The method is useful for diagnosing and/or determining
XX CC a predisposition to a cellular proliferative disorder, in particular
XX CC breast cancer including ductal carcinoma in situ, lobular carcinoma,
XX CC colloid carcinoma, tubular carcinoma, medullary carcinoma, metaplastic
XX CC carcinoma, intraductal carcinoma in situ, lobular carcinoma in situ and
XX CC papillary carcinoma in situ. The present sequence is a gene fragment used
XX CC in the exemplification of the invention.
XX
XX Sequence 1794 BP; 240 A; 646 C; 522 G; 318 T; 68 other;
XX
XX Query Match 55.1%; Score 310.4; DB 24; Length 1794;
XX Best Local Similarity 92.9%; Pred. No. 1.9e-51;
XX Matches 314; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
XX
XX QY 226 GGGGCGCGTGGGATCGAGCCGCAAGCGAGGTGGCGGCGGCTCGCGGAGAC 285
XX Db 846 GGGGCGCGTGGGATCGAGCCGCAAGCGAGGTGGCGGCGGCTCGCGGAGAC 905
XX QY 286 AAGGCGCGGCTGGCTCTCTAGAGGGCCCCCAGCGCTTGCAGAGAGAGTCTTGAGG 345
XX Db 906 AAGGCGCGGCTGGCTCTCTAGAGGGCCCCCAGCGCTTGCAGAGAGAGTCTTGAGG 965
XX QY 346 CCGGCGCGAGGAGGCGGCGGCTTCCAGCGGCGCGCGCGCGAGCAAGAGTTGGC 405
XX Db 966 CCGGCGCGAGGAGGCGGCGGCTTCCAGCGGCGCGCGCGCGAGCAAGAGTTGGC 1025
XX QY 406 CAGGCGCGCGTGGAGCGAGCGGCGGCGGCTTCTCAGAGAGCGCGGAGAGCGCGGCG 465
XX Db 1026 CAGGCGCGCGTGGAGCGAGCGGCGGCGGCTTCTCAGAGAGCGCGGAGAGCGCGGCG 1085
XX QY 466 CTGGAGGCGCGAGGAGCGGCGGTATAGAGGCTGTGGCGCTTGGCGGCGAGCGGAGTT 525
XX Db 1086 CTGGAGGCGCGAGGAGCGGCGGTATAGAGGCTGTGGCGCTTGGCGGCGAGCGGAGTT 1145
XX QY 526 CCGCGCGCGCGCGCGAGCGCGCGCGCGCATGAGAGCTGGCC 563
XX Db 1146 CCGCGCGCGCGCGCGAGCGCGCGCGCGCATGAGAGCTGGCC 1183
XX
XX RESULT 2
XX AAV54620 standard; cDNA; 562 BP.
XX
XX AC AAV54620;
XX
XX DT 25-MAR-2003 (updated);
XX DT 30-OCT-1998 (first entry)
XX
XX DE LUI05 specific consensus polynucleotide sequence.
XX
XX KW LUI05; lung disease marker; immunoassay; lung disease; cancer;
XX KM blood; plasma; serum; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers

```

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FT CDS 122..436
FT /*tag= a
FT /transl_except= (pos:176..178, aa:Val)
FT /product= "LUI05 polypeptide"
XX
XX W09833926-A1.
XX
XX PD 06-AUG-1998.
XX
XX PF 30-JAN-1998; 98WO-US01766.
XX
XX PR 31-JAN-1997; 97US-0791710.
XX
XX PA (ABBO ) ABBOTT LAB.
XX
XX PI Billing-medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertsrapp L;
XX PI Russell JC, Stroupe SD;
XX
XX WP1: 1998-437479/37.
XX
XX DR P-PSDB; AAV56868.
XX
XX PT New nucleic acid for the lung disease marker LUI05 - polypeptides,
XX PT antibodies and genes, used for diagnosis, prevention, treatment of
XX PT lung disease, specifically cancer
XX
XX Claim 11; Fig 1; 123pp; English.
XX
XX Sequences shown in AAV54616 to AAV54621 represent LUI05 specific
XX CC polynucleotide sequences. These are used in the method of the invention
XX CC for detecting target LUI05 nucleic acid. The method comprises treating a
XX CC sample with at least one LUI05 specific nucleic acid, or its complement
XX CC which is at least 50 percent identical with the LUI05 specific nucleic
XX CC acid sequences (AAV54616 to AAV54621). LUI05 is a lung disease marker.
XX CC Cells transformed with a recombinant expression system that contains
XX CC LUI05 specific nucleic acid fragments, are used to express recombinant
XX CC LUI05 polypeptides which are used to raise antibodies. The antibodies are
XX CC used to detect the LUI05 antigen, and correspondingly this antigen is
XX CC used to detect specific antibodies, in usual immunoassays. The LUI05
XX CC polypeptides and nucleic acid sequences are used for diagnosis, staging,
XX CC monitoring, prognosis, prevention, treatment and determination of
XX CC susceptibility to, lung disease, specifically cancer. The LUI05
XX CC polypeptides are also used to screen for specific binding agents, useful
XX CC therapeutically. LUI05 is a marker for lung disease (present at high
XX CC concentration, in altered form or in an unusual body compartment). LUI05
XX CC can be detected in blood, plasma or serum in an inexpensive, non-invasive
XX CC test.
XX CC
XX CC (updated on 25-MAR-2003 to correct PI field.)
XX
XX SO Sequence 562 BP; 82 A; 200 C; 192 G; 86 T; 2 other;
XX
XX Query Match 23.4%; Score 132; DB 19; Length 562;
XX Best Local Similarity 99.2%; Pred. No. 6e-17;
XX Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 431 GCAGGCGCTTCTCAGAGCGCGGCGGCGGCGCTGAGAGGCGGAGACCGGATATA 490
XX Db 1 GCAGGCGCTTCTCAGAGCGCGGCGGCGGCGGCGCTGAGAGGCGGAGACCGGATATA 60
XX QY 491 GAGGCGCTGAGCGCTTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 550
XX Db 61 GAGGCGCTGAGCGCTTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
XX QY 551 CATGAGAGCTGGCC 563
XX Db 121 CATGAGAGCTGGCC 133
XX
XX RESULT 3
XX AAV54616 standard; cDNA; 190 BP.
XX
XX AC AAV54616;

```



XX 25-MAR-2003 (updated)  
 DT 30-OCT-1998 (first entry)  
 XX  
 DE LUN05 specific polynucleotide sequence from clone 3353867.  
 XX  
 KW LUN05; lung disease marker; immunoassay; lung disease; cancer;  
 KM blood; plasma; serum; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO9833926-A1.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PF 30-JAN-1998; 98WO-US01766.  
 XX  
 PR 31-JAN-1997; 97US-0791710.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Billing-medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Granados EN, Hodges SC, Kias MR, Kratochvil JD, Robertstrapp L;  
 PI Russell JC, Stroupe SD;  
 XX  
 DR WPI; 1998-437479/37.  
 XX  
 XX New nucleic acid for the lung disease marker LUN05 - polypeptides,  
 PT antibodies and genes, used for diagnosis, prevention, treatment of  
 PT lung disease, specifically cancer  
 XX  
 XX Claim 11; Fig 1; 123p; English.  
 PS  
 XX Sequences shown in AAV54616 to AAV54621 represent LUN05 specific  
 CC polynucleotide sequences. These are used in the method of the invention  
 CC for detecting target LUN05 nucleic acid. The method comprises treating a  
 CC sample with at least one LUN05 specific nucleic acid, or its complement  
 CC which is at least 50 percent identical with the LUN05 specific nucleic  
 CC acid sequences (AAV54616 to AAV54621). LUN05 is a lung disease marker.  
 CC Cells transformed with a recombinant expression system that contains  
 CC LUN05 specific nucleic acid fragments, are used to express recombinant  
 CC LUN05 polypeptides which are used to raise antibodies. The antibodies are  
 CC used to detect the LUN05 antigen, and correspondingly this antigen is  
 CC used to detect specific antibodies, in usual immunoassays. The LUN05  
 CC polypeptides and nucleic acid sequences are used for diagnosis, staging,  
 CC monitoring prognosis, prevention, treatment and determination of  
 CC susceptibility to, lung disease, specifically cancer. The LUN05  
 CC polypeptides are also used to screen for specific binding agents, useful  
 CC therapeutically. LUN05 is a marker for lung disease (present at high  
 CC concentration in altered form or in an unusual body compartment). LUN05  
 CC can be detected in blood, plasma or serum in an inexpensive, non-invasive  
 CC test.  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 CC  
 CC Sequence 190 BP; 18 A; 69 C; 67 G; 32 T; 4 other;  
 XX  
 SQ  
 Query Match 22.9%; Score 129; DB 19; Length 190;  
 Best Local Similarity 97.0%; Pred. No. 2,4e-16;  
 Matches 129; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 431 GAGAGCTTTCTCAGAGCGCGCGAGCGCGCTGAGAGGGGAGAGCCGGGTATPA 490  
 DB 1 GAGAGCTTTCTCAGAGCGCGCGAGCGCGCGCTGAGAGGGGAGAGCCGGGTATPA 60  
 QY 491 GAGAGCTTTCTCAGAGCGCGCGAGCGCGAGTTCCCGCGCGCGCGCGCGCGC 550  
 DB 61 GAGAGCTTTCTCAGAGCGCGCGAGCGCGAGTTCCCGCGCGCGCGCGCGCGC 120  
 QY 551 GAGAGCTTTCTCAGAGCGCGCGAGCGCGAGTTCCCGCGCGCGCGCGCGCGC  
 DB 121 GAGAGCTTTCTCAGAGCGCGCGAGCGCGAGTTCCCGCGCGCGCGCGCGCGC

RESULT 4  
 ID AAZ98173 standard; CDNA; 543 BP.  
 XX  
 AC AAZ98173;  
 XX  
 DT 11-MAY-2000 (first entry)  
 XX  
 DE Human signal peptide containing protein HSP65-65 CDNA SEQ ID NO:199.  
 XX  
 KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;  
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
 KW antimicrobial; neuroprotective; cardiovascular; hepatocytic;  
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;  
 KW reproductive disorder; developmental disorder; arteriosclerosis;  
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anemia;  
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
 KW Parkinson's disease; Huntington's disease; ovulatory defect;  
 KW muscular dystrophy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200000610-A2.  
 XX  
 PD 06-JAN-2000.  
 XX  
 PF 25-JUN-1999; 99WO-US14484.  
 XX  
 XX 26-JUN-1998; 98US-0090762.  
 PR 31-JUL-1998; 98US-0094983.  
 PR 01-OCT-1998; 98US-0102686.  
 PR 11-DEC-1998; 98US-0112129.  
 XX  
 XX (INCY-) INCYTE PHARM INC.  
 XX  
 XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
 XX Akersblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
 XX Bandman O;  
 XX  
 XX WPI; 2000-160673/14.  
 DR P-PsDB; AAY87288.  
 XX  
 XX New human signal peptide-containing proteins useful in treatment,  
 PT prevention and diagnosis of e.g. cancer, inflammation and  
 PT cardiovascular disease  
 PT  
 XX  
 PS Claim 9; Page 289; 327p; English.  
 XX  
 XX AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the  
 CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have  
 CC anticancer, anti-inflammatory, antimicrobial, hepatocytic, and can  
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can  
 CC be used in gene therapy. HSPs can be used to treat or prevent disorders  
 CC associated with decreased activity or function of HSP. Antagonists of  
 CC HSP are used to treat or prevent disorders associated with increased  
 CC activity or function of HSP. Such disorders include cell proliferation  
 CC (including cancer), inflammation, cardiovascular, neurological,  
 CC reproductive or developmental disorders, e.g. arteriosclerosis,  
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, congestive or  
 CC asthma, Crohn's disease, microbial or other infections, Huntington's  
 CC disease, schizophrenia, ovulatory defects, production of HSP, for  
 CC detecting HSP in standard hybridisation and amplification assays (for  
 CC diagnosis and monitoring), in gene therapy, as detecting related sequences  
 CC or genetic variations, and for chromosomal mapping. HSP are also used to  
 CC triplex-forming or ribozyme therapeutics, for detecting HSP are also used to  
 CC raise specific antibodies (Ab) and to screen for agonists and  
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or  
 CC monitor HSP-related diseases (in usual immunoassays), as therapeutic  
 CC antagonists, in competitive drug screens, and for purification of HSP  
 CC from natural sources.  
 XX



Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGACCGGGTATAGAAAGCTTGGCTTGGCCGGGAGCGGAGGTTCCCGCGC 533  
DB 1 GCGAGACCGGGTATAGAAAGCTTGGCTTGGCCGGGAGCGGAGGTTCCCGCGC 60  
OY 534 GCGCCGAGCGCCCGCGCCATGAAAGCTCGCC 563  
DB 61 GCGCCGAGCGCCCGCGCCATGAAAGCTCGCC 90

RESULT 7  
ABK40267  
ID ABK40267 standard; cDNA: 569 BP.  
AC ABK40267;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE cDNA encoding human PRO1245 polypeptide.  
XX  
KM Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;  
KM leukemia; neuronal disorder; stromal disorder; blastocoele disorder;  
KM inflammatory disorder; immune disorder; angiogenic disorder;  
KM gene therapy; cyostatic; neuroprotective; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200153486-A1.  
PD 26-JUL-2001.  
PF 11-FEB-2000; 2000WO-US03565.  
XX  
XX 08-MAR-1999; 99WO-US05028.  
PR 11-MAR-1999; 98US-123972P.  
PR 11-MAY-1999; 98US-133459P.  
PR 02-JUN-1999; 98WO-US12252.  
PR 22-JUN-1999; 98US-140650P.  
PR 22-JUN-1999; 98US-140653P.  
PR 20-JUL-1999; 98US-144756P.  
PR 26-JUL-1999; 98US-145698P.  
PR 28-JUL-1999; 98US-146222P.  
PR 17-AUG-1999; 99US-149382P.  
PR 31-AUG-1999; 99WO-US20111.  
PR 01-SEP-1999; 99WO-US21030.  
PR 15-SEP-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 01-DEC-1999; 99WO-US28634.  
PR 05-JAN-2000; 2000WO-US00219.  
XX  
XX (GETH ) GENENTECH INC.  
PA Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;  
PI Marshers SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;  
PI Matanabe CK, Wood WI;  
XX  
DR WPI; 2002-205567/26.  
XX P-PSDB; AAU86141.  
XX  
XX Thirty five nucleic acids encoding PRO polypeptides, useful for  
PT treating benign or malignant tumours, leukemias and lymphoid  
PT malignancies, inflammatory, angiogenic and immunologic disorders -  
XX  
XX Claim 50; Fig 27; 302PP; English.  
XX  
XX The present invention relates to the isolation of novel human PRO  
CC polypeptides and the polynucleotide sequences encoding them. The  
CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are  
CC useful for treating benign or malignant tumours (e.g. renal, kidney,  
CC bladder, breast, etc), leukemias and lymphoid malignancies, other  
CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,

CC macrophagal, stromal and blastocoele disorders, inflammatory, immune  
CC and angiogenic disorders. The polynucleotide sequences are also  
CC useful in gene therapy. ABK40267-ABK40288 encode for the human PRO  
CC polypeptides of the invention.  
XX  
SQ Sequence 569 BP; 128 A; 190 C; 170 G; 81 T; 0 other;

Query Match 16.0%; Score 90; DB 24; Length 569;  
Best Local Similarity 100.0%; Pred. No. 7.9e-09;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGACCGGGTATAGAAAGCTTGGCTTGGCCGGGAGCGGAGGTTCCCGCGC 533  
DB 1 GCGAGACCGGGTATAGAAAGCTTGGCTTGGCCGGGAGCGGAGGTTCCCGCGC 60  
OY 534 GCGCCGAGCGCCCGCGCCATGAAAGCTCGCC 563  
DB 61 GCGCCGAGCGCCCGCGCCATGAAAGCTCGCC 90

RESULT 8  
AAZ65103  
ID AAZ65103 standard; cDNA: 570 BP.  
AC AAZ65103;  
XX  
DT 05-APR-2000 (first entry)  
XX  
DE Membrane-bound protein PRO1245 encoding cDNA.  
XX  
DE Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KM pharmaceutical; receptor immunoadhesin; gene mapping; ss.  
XX  
XX Homo sapiens.  
XX  
PN WO9963088-A2.  
PD 09-DEC-1999.  
PF 02-JUN-1999; 99WO-US12252.  
XX  
XX 02-JUN-1998; 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
PR 02-JUN-1998; 98US-0087627.  
PR 03-JUN-1998; 98US-0088021.  
PR 04-JUN-1998; 98US-0088025.  
PR 04-JUN-1998; 98US-0088028.  
PR 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
PR 04-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088217.  
PR 05-JUN-1998; 98US-0088655.  
PR 09-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
PR 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
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PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088865.  
PR 11-JUN-1998; 98US-0088876.

PR 12-JUN-1998; 98US-0089090.  
PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089650.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 22-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090258.  
PR 23-JUN-1998; 98US-0090254.  
PR 23-JUN-1998; 98US-0090348.  
PR 23-JUN-1998; 98US-0090349.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090433.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.  
PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 25-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090676.  
PR 25-JUN-1998; 98US-0090678.  
PR 25-JUN-1998; 98US-0090680.  
PR 25-JUN-1998; 98US-0090690.  
PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.  
PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
PR 01-JUL-1998; 98US-0091358.  
PR 01-JUL-1998; 98US-0091360.  
PR 01-JUL-1998; 98US-0091544.  
PR 02-JUL-1998; 98US-0091478.  
PR 02-JUL-1998; 98US-0091486.  
PR 02-JUL-1998; 98US-0091512.  
PR 02-JUL-1998; 98US-0091628.  
PR 02-JUL-1998; 98US-0091628.  
PR 02-JUL-1998; 98US-0091633.  
PR 02-JUL-1998; 98US-0091646.  
PR 07-JUL-1998; 98US-0091673.  
PR 07-JUL-1998; 98US-0091982.  
PR 09-JUL-1998; 98US-0092182.  
PR 10-JUL-1998; 98US-0092472.  
PR 30-JUL-1998; 98US-0093339.  
PR 04-AUG-1998; 98US-0094651.  
PR 04-AUG-1998; 98US-0095282.  
PR 04-AUG-1998; 98US-0095285.  
PR 04-AUG-1998; 98US-0095301.  
PR 04-AUG-1998; 98US-0095302.  
PR 04-AUG-1998; 98US-0095318.  
PR 04-AUG-1998; 98US-0095321.  
PR 10-AUG-1998; 98US-0095325.  
PR 10-AUG-1998; 98US-0095916.  
PR 10-AUG-1998; 98US-0095929.  
PR 10-AUG-1998; 98US-0096102.  
PR 11-AUG-1998; 98US-0096143.  
PR 12-AUG-1998; 98US-0096146.  
PR 12-AUG-1998; 98US-0096329.

PR 17-AUG-1998; 98US-0096757.  
PR 17-AUG-1998; 98US-0096766.  
PR 17-AUG-1998; 98US-0096768.  
PR 17-AUG-1998; 98US-0096773.  
PR 17-AUG-1998; 98US-0096791.  
PR 17-AUG-1998; 98US-0096867.  
PR 17-AUG-1998; 98US-0096891.  
PR 17-AUG-1998; 98US-0096894.  
PR 17-AUG-1998; 98US-0096895.  
PR 17-AUG-1998; 98US-0096897.  
PR 18-AUG-1998; 98US-0096949.  
PR 18-AUG-1998; 98US-0096950.  
PR 18-AUG-1998; 98US-0096959.  
PR 18-AUG-1998; 98US-0096960.  
PR 18-AUG-1998; 98US-0097022.  
PR 19-AUG-1998; 98US-0097141.  
PR 20-AUG-1998; 98US-0097218.  
PR 24-AUG-1998; 98US-0097661.  
PR 26-AUG-1998; 98US-0097951.  
PR 26-AUG-1998; 98US-0097952.  
PR 26-AUG-1998; 98US-0097954.  
PR 26-AUG-1998; 98US-0097955.  
PR 26-AUG-1998; 98US-0097971.  
PR 26-AUG-1998; 98US-0097974.  
PR 26-AUG-1998; 98US-0097978.  
PR 26-AUG-1998; 98US-0097979.  
PR 26-AUG-1998; 98US-0097986.  
PR 26-AUG-1998; 98US-0098014.  
PR 31-AUG-1998; 98US-0098525.  
PR 16-SEP-1998; 98US-0100634.  
PR 12-JAN-1999; 98US-0115565.  
PR (GENTH ) GENENTECH INC.  
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
XX WPI; 2000-072883/06.  
DR P-PSDB; AAY66757.  
XX Membrane-bound proteins and related nucleotide sequences -  
PT Claim 2; Fig 289; 822pp; English.  
XX The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC ligands have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.  
SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;  
Query Match 16.0%; Score 90; DB 21; Length 570;  
Best Local Similarity 100.0%; Pred. No. 7.9e-09;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 474 GCGAGACCGCGGTATTAAGAACCTCTGCGCTTCCCGGACCGCCAGATTCCCGCGC 533  
Db 1 GCGAGACCGCGGTATTAAGAACCTCTGCGCTTCCCGGACCGCCAGATTCCCGCGC 60  
QY 534 GCCCGAGCGCGCGCGCCATGAGCTCGCC 563  
Db 61 GCCCGAGCGCGCGCGCCATGAGCTCGCC 90

RESULT 9  
AAFA4249 standard; cDNA; 570 BP.  
XX  
XX AAF44249;  
AC  
XX 02-APR-2001 (first entry)  
XX  
XX Human PRO1245 (UNQ629) nucleotide sequence SEQ ID NO:407.  
XX  
XX Human, secreted and transmembrane protein; PRO; cytosolic;  
XX cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
XX diagnostic assay; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200073454-A1.  
XX  
XX 07-DEC-2000.  
XX  
XX 30-MAR-2000; 2000WO-US08439.  
XX  
XX 02-JUN-1999; 99WO-US12252.  
XX 23-JUN-1999; 99US-0141037.  
XX 07-JUL-1999; 99US-0143048.  
XX 20-JUL-1999; 99US-0144758.  
XX 26-JUL-1999; 99US-0145698.  
XX 28-JUL-1999; 99US-0146222.  
XX 17-AUG-1999; 99US-0149396.  
XX 15-SEP-1999; 99WO-US21509.  
XX 08-OCT-1999; 99US-0158663.  
XX 30-NOV-1999; 99WO-US28313.  
XX 01-DEC-1999; 99WO-US28301.  
XX 16-DEC-1999; 99WO-US30911.  
XX 20-DEC-1999; 99WO-US30911.  
XX 05-JAN-2000; 2000WO-US00219.  
XX 06-JAN-2000; 2000WO-US00376.  
XX 11-FEB-2000; 2000WO-US03565.  
XX 18-FEB-2000; 2000WO-US04341.  
XX 22-FEB-2000; 2000WO-US04914.  
XX 24-FEB-2000; 2000WO-US04914.  
XX 02-MAR-2000; 2000WO-US05004.  
XX 15-MAR-2000; 2000WO-US06884.  
XX 20-MAR-2000; 2000WO-US07377.  
XX  
XX (GENT) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers IJ, Eaton DL;  
XX Petrára N, Fong S, Geider H, Gerritsen ME, Goddard A, Godowski PJ;  
XX Grimaldi CJ, Gurney AL, Kijavich IT, Napier MA, Pan J, Paoni NF;  
XX Roy MA, Stewart TA, Tumas D, Watanabe CX, Williams PM, Wood WT;  
XX Zhang Z;  
XX  
XX WPI; 2001-032160/04.  
XX P-PSDB; AAB65280.  
XX  
XX PRO polynucleotides used to produce polypeptides used to target  
XX bioactive molecules such as toxins, radiolabels or antibodies, to  
XX specific cells, to cause targeted cell death -  
XX  
XX Claim 2: Fig 289; 935pp; English.  
XX  
XX The present invention describes human secreted and transmembrane PRO  
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins  
XX can be used for targeted delivery of bioactive molecules, that cause cell death. PRO nucleotide  
XX toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
XX sequences, and their fragments, can be used as hybridisation probes in  
XX chromosomal and gene mapping, and in the generation of anti-sense RNA  
XX and DNA. They may also be used to produce transgenic animals which are  
XX used to develop and screen therapeutically useful reagents. The PRO

CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF4270 to AAF4470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF4087 to AAF4269 and  
CC AAB6154 to AAB6300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
XX Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;  
XX  
XX Query Match 16.0%; Score 90; DB 22; Length 570;  
XX Best Local Similarity 100.0%; Pred. No. 7.9e-09;  
XX Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 474 GCGAGACCGGGTATATAGAGCCCTGTGACCTTGCCTGCGAGCGCAGATTCCCGCGC 533  
XX 1 GCGAGACCGGGTATATAGAGCCCTGTGACCTTGCCTGCGAGCGCAGATTCCCGCGC 60  
XX  
XX QY 534 GCGCGAGCGCGCGCGCCATGAGCTCGCC 563  
XX 61 GCGCGAGCGCGCGCGCCATGAGCTCGCC 90  
XX  
XX Db  
XX  
XX RESULT 10  
XX AAB80386  
XX ID AAB80386 standard; DNA; 570 BP.  
XX  
XX AAB80386;  
XX  
XX 28-APR-2003 (first entry)  
XX  
XX Novel human secreted or transmembrane protein PRO1358 DNA.  
XX  
XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
XX cardiac insufficiency disorder; cancer; tumour; immune response;  
XX adrenal cortical capillary endothelial growth; c-fos induction;  
XX vascular endothelial growth factor inhibition; VEGF inhibition;  
XX endothelial cell growth inhibitor; T-lymphocytes stimulation;  
XX retinal neurons cell survival; rod photoreceptor cell survival;  
XX retinal disorder; retinitis pigmentosa; kidney disease;  
XX mammalian kidney mesangial cell proliferation; Berger disease;  
XX dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
XX chondrocyte redifferentiation; sports injury; arthritis; gene; de..  
XX  
XX Homo sapiens.  
XX  
XX US2002132252-A1.  
XX  
XX 19-SEP-2002.  
XX  
XX 14-NOV-2001; 2001US-0990442.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
XX 16-SEP-1998; 98WO-US19330.  
XX 17-SEP-1998; 98WO-US19437.  
XX 07-OCT-1998; 98WO-US21141.  
XX 01-DEC-1998; 98WO-US25108.  
XX 05-JAN-1999; 99WO-US01006.  
XX 08-MAR-1999; 99WO-US05028.  
XX 02-JUN-1999; 99WO-US12252.  
XX 15-SEP-1999; 99WO-US21090.  
XX 15-SEP-1999; 99WO-US21547.  
XX 30-NOV-1999; 99WO-US28313.  
XX 01-DEC-1999; 99WO-US28301.  
XX 16-DEC-1999; 99WO-US28634.  
XX 20-DEC-1999; 99WO-US30095.  
XX 06-JAN-2000; 2000WO-US00376.  
XX 11-FEB-2000; 2000WO-US03565.  
XX 18-FEB-2000; 2000WO-US04341.  
XX 22-FEB-2000; 2000WO-US04914.  
XX 24-FEB-2000; 2000WO-US04914.  
XX

PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 15-MAY-2000; 2000WO-US13358.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUN-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23542.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 06-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 28-FEB-2001; 2001WO-US32678.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 02-JUN-2001; 2001WO-US21066.  
 PR 16-JUN-2001; 2001WO-US21735.  
 PR 12-OCT-1997; 97US-049787P.  
 PR 12-OCT-1997; 97US-062250P.  
 PR 12-NOV-1997; 97US-065311P.  
 PR 24-NOV-1997; 97US-066770P.  
 PR 25-FEB-1998; 98US-075945P.  
 PR 20-MAR-1998; 98US-078910P.  
 PR 28-APR-1998; 98US-083322P.  
 PR 07-MAY-1998; 98US-084600P.  
 PR 28-MAY-1998; 98US-087106P.  
 PR 02-JUN-1998; 98US-087607P.  
 PR 02-JUN-1998; 98US-087609P.  
 PR 02-JUN-1998; 98US-087759P.  
 PR 03-JUN-1998; 98US-088021P.  
 PR 04-JUN-1998; 98US-088025P.  
 PR 04-JUN-1998; 98US-088026P.  
 PR 04-JUN-1998; 98US-088028P.  
 PR 04-JUN-1998; 98US-088029P.  
 PR 04-JUN-1998; 98US-088030P.  
 PR 04-JUN-1998; 98US-088033P.  
 PR 04-JUN-1998; 98US-088326P.  
 PR 05-JUN-1998; 98US-088327P.  
 PR 05-JUN-1998; 98US-088328P.  
 PR 05-JUN-1998; 98US-088317P.  
 PR 09-JUN-1998; 98US-088555P.  
 PR 10-JUN-1998; 98US-088734P.  
 PR 10-JUN-1998; 98US-088736P.  
 PR 10-JUN-1998; 98US-088742P.  
 PR 10-JUN-1998; 98US-088810P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 11-JUN-1998; 98US-088826P.  
 PR 11-JUN-1998; 98US-088858P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 12-JUN-1998; 98US-088876P.  
 PR 16-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089140P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 17-JUN-1998; 98US-089532P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089598P.  
 PR 17-JUN-1998; 98US-089599P.  
 PR 17-JUN-1998; 98US-089600P.  
 PR 18-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089907P.  
 PR 28-AUG-2001; 2001US-094192P.  
 XX  
 XX  
 (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Borstein D, Desnoyers L, Eaton DL,  
 PI Ferrera N, Fong S, Gerber H, Gettleman ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurley AL, Kiljavin IU, Napier MA, Pan J, Paoletti NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;  
 DR WPI: 2003-247083/24.  
 DR P-15DB; AB059174.  
 XX  
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT are therapeutically useful for enhancing immune response and in cancer  
 PT treatments  
 XX  
 PS Claim 2; Fig 291; 648bp; English.  
 XX  
 CC The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting human PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
 CC stimulate adrenal cortical capillary endothelial growth and PRO326,  
 CC PRO993, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and angiogenesis of this polypeptide are  
 CC useful for treating cancerous tumours. PRO812 inhibits proliferation of  
 CC endothelial growth factor (VEGF) stimulated endothelial cell growth in  
 CC cells and is thus useful for inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
 CC immune response. PRO828, PRO1068 or PRO1375 stimulate proliferation of  
 CC retinal neurons cells (PRO1132) and also enhances survival/proliferation of  
 CC rod photoreceptor cells and therefore are useful for treating retinal  
 CC disorders of injuries e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpetic stomatitis or Crohn's  
 CC disease. PRO1310, PRO864, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or differentiation of chondrocytes in culture and  
 CC are thus useful for treating sports injuries, and arthritis. This  
 CC sequence represents a novel human PRO protein polynucleotide.  
 XX  
 SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;  
 Query Match 16.0%; Score 90; DB 25; Length 570;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-09;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 474 GCGAGACCGGGTATAGAAAGCTCTGCTGCGCGGAGCGGACAGTTCCCGGCG 533  
 Db 1 GCGAGACCGGGTATAGAAAGCTCTGCTGCGCGGAGCGGACAGTTCCCGGCG 60  
 QY 534 GCCCGGAGCGCGCGCGCCATGAAGCTCGCC 563  
 Db 61 GCCCGGAGCGCGCGCGCCATGAAGCTCGCC 90  
 RESULT 11  
 ABX80890  
 ID ABX80890 standard; cDNA; 570 BP.  
 AC ABX80890;  
 XX  
 XX 22-APR-2003 (first entry)  
 DT Human secreted/transmembrane protein cDNA, #163.  
 XX Human secreted/transmembrane protein cDNA, #163.  
 DE Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
 XX  
 KM

KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW gene therapy; tumour-associated antigenic target; TAR; ADAPT;  
KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
OS Homo sapiens.  
XX US2003027162-A1.  
XX PD 06-FEB-2003.  
XX 15-NOV-2001; 2001US-0997428.  
XX 05-NOV-1997; 97WO-US20069.  
XX 16-SEP-1998; 98WO-US19330.  
XX 17-SEP-1998; 98WO-US19347.  
XX 07-OCT-1998; 98WO-US21141.  
XX 01-DEC-1998; 98WO-US25108.  
XX 05-JAN-1999; 99WO-US00106.  
XX 08-MAR-1999; 99WO-US05028.  
XX 02-JUN-1999; 99WO-US12252.  
XX 15-SEP-1999; 99WO-US21090.  
XX 15-SEP-1999; 99WO-US21547.  
XX 30-NOV-1999; 99WO-US28313.  
XX 01-DEC-1999; 99WO-US28301.  
XX 01-DEC-1999; 99WO-US28634.  
XX 16-DEC-1999; 99WO-US30095.  
XX 20-DEC-1999; 99WO-US30911.  
XX 05-JAN-2000; 2000WO-US00219.  
XX 06-JAN-2000; 2000WO-US00376.  
XX 11-FEB-2000; 2000WO-US03365.  
XX 18-FEB-2000; 2000WO-US04341.  
XX 24-FEB-2000; 2000WO-US04914.  
XX 24-FEB-2000; 2000WO-US05004.  
XX 02-MAR-2000; 2000WO-US05841.  
XX 10-MAR-2000; 2000WO-US06319.  
XX 15-MAR-2000; 2000WO-US06884.  
XX 30-MAR-2000; 2000WO-US07377.  
XX 15-MAY-2000; 2000WO-US13358.  
XX 17-MAY-2000; 2000WO-US13705.  
XX 22-MAY-2000; 2000WO-US14042.  
XX 30-MAY-2000; 2000WO-US14941.  
XX 02-JUN-2000; 2000WO-US20710.  
XX 11-AUG-2000; 2000WO-US23352.  
XX 23-AUG-2000; 2000WO-US23352.  
XX 08-NOV-2000; 2000WO-US32678.  
XX 01-DEC-2000; 2000WO-US32678.  
XX 28-FEB-2001; 2001WO-US17800.  
XX 01-JUN-2001; 2001WO-US19692.  
XX 20-JUN-2001; 2001WO-US21066.  
XX 09-JUL-2001; 2001WO-US21735.  
XX 16-JUN-1997; 97US-049787P.  
XX 17-OCT-1997; 97US-062250P.  
XX 12-NOV-1997; 97US-065111P.  
XX 13-NOV-1997; 97US-065770P.  
XX 24-NOV-1997; 98US-075945P.  
XX 25-FEB-1998; 98US-078910P.  
XX 20-MAR-1998; 98US-083322P.  
XX 28-APR-1998; 98US-084600P.  
XX 07-MAY-1998; 98US-087106P.  
XX 28-MAY-1998; 98US-087607P.  
XX 02-JUN-1998; 98US-087609P.  
XX 02-JUN-1998; 98US-087759P.  
XX 03-JUN-1998; 98US-088021P.  
XX 04-JUN-1998; 98US-088025P.  
XX 04-JUN-1998; 98US-088026P.  
XX 04-JUN-1998; 98US-088028P.

PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088126P.  
PR 05-JUN-1998; 98US-088167P.  
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PR 05-JUN-1998; 98US-088212P.  
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PR 09-JUN-1998; 98US-088655P.  
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PR 10-JUN-1998; 98US-088738P.  
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PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
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PR 16-JUN-1998; 98US-089514P.  
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PR 19-JUN-1998; 98US-089952P.  
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PR 23-JUN-1998; 98US-090355P.  
PR 24-JUN-1998; 98US-090429P.  
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PR 24-JUN-1998; 98US-090435P.  
PR 24-JUN-1998; 98US-090444P.  
PR 24-JUN-1998; 98US-090445P.  
PR 24-JUN-1998; 98US-090472P.  
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PR 24-JUN-1998; 98US-090542P.  
PR 24-JUN-1998; 98US-090549P.  
PR 24-JUN-1998; 98US-090576P.  
PR 25-JUN-1998; 98US-090678P.  
PR 25-JUN-1998; 98US-090690P.  
PR 25-JUN-1998; 98US-090694P.  
PR 25-JUN-1998; 98US-090695P.  
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PR 26-JUN-1998; 98US-090863P.  
PR 26-JUN-1998; 98US-091360P.  
PR 01-JUL-1998; 98US-091478P.  
PR 01-JUL-1998; 98US-091544P.  
PR 02-JUL-1998; 98US-091549P.  
PR 02-JUL-1998; 98US-091626P.  
PR 02-JUL-1998; 98US-091638P.  
PR 02-JUL-1998; 98US-091643P.  
PR 02-JUL-1998; 98US-091647P.  
PR 02-JUL-1998; 98US-091978P.  
PR 07-JUL-1998; 98US-091979P.  
PR 07-JUL-1998; 98US-092172P.  
PR 09-JUL-1998; 98US-092173P.  
PR 10-JUL-1998; 98US-092333P.  
PR 30-JUL-1998; 98US-094532P.  
PR 04-AUG-1998; 98US-095282P.

PR 04-AUG-1998; 98US-095285P.  
PR 04-AUG-1998; 98US-095301P.  
PR 04-AUG-1998; 98US-095302P.  
PR 04-AUG-1998; 98US-095318P.  
PR 04-AUG-1998; 98US-095321P.  
PR 04-AUG-1998; 98US-095325P.  
PR 10-AUG-1998; 98US-095316P.  
PR 10-AUG-1998; 98US-095329P.  
PR 10-AUG-1998; 98US-096012P.  
PR 11-AUG-1998; 98US-096143P.  
PR 11-AUG-1998; 98US-096146P.  
PR 12-AUG-1998; 98US-096329P.  
PR 17-AUG-1998; 98US-096757P.  
PR 17-AUG-1998; 98US-096766P.  
PR 17-AUG-1998; 98US-096773P.  
PR 17-AUG-1998; 98US-096779P.  
PR 17-AUG-1998; 98US-096867P.  
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PR 17-AUG-1998; 98US-096895P.  
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PR 18-AUG-1998; 98US-096949P.  
PR 18-AUG-1998; 98US-096950P.  
PR 18-AUG-1998; 98US-096950P.  
PR 18-AUG-1998; 98US-096950P.  
PR 18-AUG-1998; 98US-097022P.  
PR 19-AUG-1998; 98US-097141P.  
PR 20-AUG-1998; 98US-097218P.  
PR 20-AUG-1998; 98US-097261P.  
PR 20-AUG-1998; 98US-097352P.  
PR 20-AUG-1998; 98US-097354P.  
PR 20-AUG-1998; 98US-097355P.  
PR 20-AUG-1998; 98US-097371P.  
PR 20-AUG-1998; 98US-097378P.  
PR 20-AUG-1998; 98US-097379P.  
PR 20-AUG-1998; 98US-097986P.  
PR 26-AUG-1998; 98US-098014P.  
PR 26-AUG-1998; 98US-098014P.  
PR 16-SEP-1998; 98US-100634P.  
PR 17-SEP-1998; 98US-100858P.  
PR 22-DEC-1998; 98US-113296P.  
PR 12-MAR-1999; 98US-123957P.  
PR 23-JUN-1999; 98US-141037P.

Query Match  
Best Local Similarity 16.0%; Score 90; DB 25; Length 570;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAGAGCCCTCGGCGCTTCCCGGCGACCCGAGTTCCCGCGC 533  
DB 1 GCGAGGACCGGGTATAGAGCCCTCGGCGCTTCCCGGCGACCCGAGTTCCCGCGC 60  
QY 534 GCGCGGAGCCCGCGCGCATGAGCTGCGC 563  
DB 61 GCGCGGAGCCCGCGCGCATGAGCTGCGC 90

RESULT 12  
ABX81273  
ID ABX81273 standard; DNA; 570 BP.  
XX AC ABX81273;  
XX DT 22-APR-2003 (first entry)  
XX DE Novel human secreted or transmembrane protein PRO1358 DNA.  
XX KM Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KM cardiac insufficiency disorder; cancer; tumour; immune response;  
KM adrenal cortical capillary endothelial growth; c-fos induction;  
KM vascular endothelial growth factor inhibition; VEGF inhibition;

KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpetic stomatitis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
OS Homo sapiens.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
PF 14-NOV-2001; 2001US-0990562.  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US28634.  
PR 20-DEC-1999; 99WO-US30095.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUN-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23322.  
PR 09-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 26-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 29-JUN-2001; 2001WO-US19692.  
PR 09-JUL-2001; 2001WO-US21066.  
PR 16-JUN-1997; 97US-049787P.  
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PR 13-NOV-1997; 97US-065111P.  
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PR 04-JUN-1998; 98US-088021P.









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Query Match 16.0%; Score 90; DB 25; Length 570;  
Best Local Similarity 100.0%; Pred. No. 7.9e-09;  
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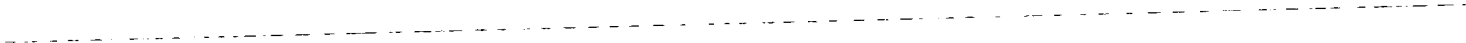
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XX
DT 17-APR-2003 (first entry)
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XX
KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;
KM pharmaceutical; diagnostic; biosensor; bioindicator; tumour; therapeutic;
KW colon cancer; lung cancer; breast cancer;cancer; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002142961-A1.
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PD 03-OCT-2002.
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PF 19-NOV-2001; 2001US-0989721.
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PR 17-SEP-1998; 98WO-US19437.
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PR 15-MAY-2000; 2000WO-US08439.
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PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US23095.
PR 08-NOV-2000; 2000WO-US23267.
PR 28-FEB-2001; 2001WO-US06520.
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PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 16-JUN-1997; 97US-049780P.
PR 17-OCT-1997; 97US-063250P.
PR 12-NOV-1997; 97US-065186P.
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PR 25-FEB-1998; 98US-075945P.
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 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.  
 (GENT) GENENTECH INC.  
 Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferreira N, Fong S, Gerlitsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Kijavitsin RJ, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 DR WPI; 2003-155950/15.  
 P-PSDB; ABUS9026.  
 XX New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
 PT PRO361 or PRO846) useful as targets for therapeutic intervention in  
 PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers  
 PT  
 PT  
 PT  
 PS Claim 2; Fig 289; 647p; English.  
 XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors, for detecting or treating e.g. tumours in  
 CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or  
 CC rabbits as targets for therapeutic intervention in certain cancers (e.g.  
 CC colon, lung or breast cancers) and diagnostic determination of the  
 CC presence of these cancers. The PRO polypeptides are also useful as  
 CC molecular weight markers or for chromosome identification. The PRO genes

CC are useful as hybridisation probes or for screening libraries of human  
 CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
 CC therapy, particularly for replacing a defective gene. The sequences  
 CC presented in ABX79290-ABX79675 are the genes encoding the primers  
 CC amplifying and the probes detecting the PRO polynucleotides of the  
 CC invention.  
 CC Note: The sequence data for this patent is also available in electronic  
 CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
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 SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;  
 Query Match 16.0%; Score 90; DB 25; Length 570;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-09; Indels 0; Gaps 0;  
 Matches 90; Conservative 0; Mismatches 0;  
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 Job time : 228 secs



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Fri Nov 7 08:48:28 2003

us-10-081-817a-19-plus-1-12-of-seq3.rnt

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
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Pred. No. is the number of results predicted by chance to have a  
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SUMMARIES

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ALIGNMENTS

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Sequence 407, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Genger, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC3  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: US/09/996,243  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28





PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

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## RESULT 2

PCT-US91-06532-1/c  
Sequence 1, Application PC/TUS9106532  
GENERAL INFORMATION:  
APPLICANT: Roizman, Bernard  
TITLE OF INVENTION: Recombinant Herpes Simplex Viruses  
TITLE OF INVENTION: Vaccines and Methods  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Bicknell  
STREET: Two First National Plaza Suite 2100  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/06532  
FILING DATE: 19910910  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Gruber, Lewis S.  
REGISTRATION NUMBER: 30,060  
REFERENCE/DOCKET NUMBER: 27373/8235  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/346-5750  
TELEFAX: 312/984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ. ID NO. 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1335 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US91-06532-1

Query Match 8.8%; Score 49.4; DB 5; Length 1335;  
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## RESULT 3

US-09-103-840A-2  
Sequence 2, Application US/09103840A  
Patent No. 6284328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
TITLE OF INVENTION: TUBERCULOSIS  
FILE REFERENCE: 24366-20007.00  
CURRENT APPLICATION NUMBER: US/09/103,840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ. ID NOS: 2  
SOFTWARE: Patent Ver. 2.1  
SEQ. ID NO. 2  
LENGTH: 4403765  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
OTHER INFORMATION: CDC 1551  
OTHER INFORMATION: "n" bases at various positions throughout the sequence  
OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 8.7%; Score 48.8; DB 3; Length 4403765;  
Best Local Similarity 46.7%; Pred. No. 0.079;  
Matches 231; Conservative 0; Mismatches 253; Indels 11; Gaps 2;

QY 1 CGCGCGGAGGCGCGCGGAGTGAAGCTGATGCTCTGCGCTTCACTCCCGAG 60  
DB 84109 CGCGAGCGCGCGCGCGCGCGCGCGCGCTCCACGAGCTGCGCGCGCGCGCGCGCG 841168

QY 61 CGCAGAGCGCGCGCGCGAGACCGCCAGTGCACGCTTGCACGCTCTGGATCAGAG 120  
DB 841169 CGCGCGCGCGAGAAACCGCAGCTGCTTGGCGCGCGCGCGCGCGCGCGCTGCGCG 841228

QY 121 CAGGACCGAGGACCGAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 180  
DB 841229 ATTCTGAAAGCGCGTGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 841288

QY 181 CCTTACNAGAGAACTCCCTTCAACCGCGC---CAGCGCTGAGGGGGGGCGTGG 237  
DB 841289 TGGCGCGAGAGAGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 841348

QY 238 GTCAGACCGCAAGCGAGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 297  
DB 841349 GCGCGCGCGCAACCGCGGAGCTGCGCACTGTATATAGCGGCGCGCGGAGCGCGG 841408

QY 298 TGCTCTCTTCAAGAGGCGCGCGCTTGCAGAGAGAACTCTCGAGGCGCGCGGAGGA 357  
DB 841409 CGCTAGTCGAGCGGAGGATTTGCGCGGAGCGAGCGGAGCGGAGCGGAGCGGAGT 841468

QY 358 AGGAGGACCGGCTTCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412

Accession	Sequence	Position
D81469	CTTCGGGTCGGGGGCTCCGGGGCGCCCGCGCGCATTTGTTGAAGCGTCGGGGACCGCGC	841528
QY413	---CGGCGCTGAGCGGAGCGGGAGGCGCTTCTCAGAGCGCGGGCGAGCGCGCGCTG	469
D841529	CGCGGGGGGGCGCGGGGGCGCCCGGGTGTATCGGCAACGCGGGCAACGCGGGCAACGG	841588
QY470	AGGCGCGAGGACCTGG	484
D841589	CGGCGCGAGCACCGG	841603

RESULT 4  
US-09-13

US-09-128-155-16/c	
Sequence 16, Application	US/09128155
Patent No. 6117654	
GENERAL INFORMATION:	
APPLICANT: Pan, Yang	
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY	
TITLE OF INVENTION: AND USES THEREOF	
FILE REFERENCE: 09404/052001	
CURRENT APPLICATION NUMBER: US/09/128,155	
CURRENT FILING DATE: 1998-08-03	
EARLIER APPLICATION NUMBER: US 60/091,650	
EARLIER FILING DATE: 1998-07-02	
EARLIER APPLICATION NUMBER: US 60/054,646	
EARLIER FILING DATE: 1997-08-04	
NUMBER OF SEQ ID NOS: 18	
SOFTWARE: FastSeq for Windows Version 3.0	
SEQ ID NO 152331	
LENGTH: 152331	
TYPE: DNA	
ORGANISM: Homo sapiens	
FEATURES:	
NAME/KEY: misc_feature	
LOCATION: (1)..(152331)	
OTHER INFORMATION: n = A,T,C or G	
US-09-128-155-16	

	Query Match	Best Local Similarity	8.6%; Score 48.6; DB 3; Length 152331;	49.8%; Pred. No. 0.078;	Matches 151; Conservative 0; Mismatches 149; Indels 3; Gaps 1;
Qy	221	GCAGGGGGGGCGTGGGGGTGAGACCCGGAAGGCAAGTGGCGGGCCGGGGTGGCCCTTCGGG	280		
Db	22234	GCTGGGGGGGGGGGGGTGGGGGCTGGGGGCTGGCCGGCCGGCGGGGGGGGGGGGGGGGGGGGGGG	22175		
Qy	281	GAGACAAAGCCCGGGCTTGCTCTCTCAGAGGGCCCCAGCGCTGCAGAGAGAACTCT	340		
Db	22174	GCGGGGGGGCGGGGGGGGGGTCTGGGGGGTGGCGGGCGGGGCGGGGGGGGGGGGGGGGGGGGGGG	22115		
Qy	341	CGAGGGCCCGGGCGAGGAAAGGGGGGCGAGGGCTTCCAGAGCGCGCCCGGGCGCAGAGGAAG	400		
Db	22114	TGCGGGGGGGGGGGGGGGGGGGCGGGGGCGCTCGAGGGTGGGGGGGTGGCTTGGAGCCGAGTGGGGG	22055		
Qy	401	TTGGCCAGGGCGACCGCCCTGAGCGCGAGCGGGCGAGGGCTTCTCAGAGATCGCGGCGAGGC	460		
Db	22054	GTTGG--GG	21998		
Qy	461	CGCGCGCTGAGAGGGGCGAGACCGGGTAAAGAACTCTGTGGCTTGGCCCGGGCAGCGCC	520		
Db	21997	CGGGGGCGGG	21938		
Qy	521	AGG 523			
Db	21937	GGG 21935			

## RESULT 5

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US-09-103-840A-1 |
; Sequence 1, Application US/09103840A |
; Patent No. 6294328 |
; GENERAL INFORMATION: |
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1  APPLICANT: FLEISCHMAN, Robert D.
2  APPLICANT: WHITE, Owen R.
3  APPLICANT: FRASER, Claire M.
4  APPLICANT: VENTER, John C.
5  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
6  TITLE OF INVENTION: TUBERCULOSIS
7  FILE REFERENCE: 24366-20007.00
8  CURRENT APPLICATION NUMBER: US/09/103,840A
9  CURRENT FILING DATE: 1998-06-24
10 NUMBER OF SEQ ID NOS: 2
11 SOFTWARE: Patentln Ver. 2.1
12 SEQ ID NO. 1
13 LENGTH: 4411529
14 TYPE: DNA
15 ORGANISM: Mycobacterium tuberculosis
16 OTHER INFORMATION: H37Rv
17 US-09-103-840A-1

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Query Match	8.6%;	Score 48.4;	DB 3;	Length 4411529;
Best Local Similarity	47.9%;	Pred. No. 0.095;		
Matches 237;	Conservative	0;	Mismatches 247;	Indels 11;
				Gaps 3

OY	1	CGCGCGGGGAGGCGCGCGGAACTGAGGCGCTGATCGTCCCTTGCGCCCTCAACTTCCAGG	60
Db	838931	CGGCACCGCGCGGGCGGGGGGCGCTCCACCGACGTGCGCGGCGGGGCGGGTGGGCGCGG	838990
OY	61	CGCAGAAAGCGGCCCAAGAGACCCCACTGCGCCGACGTTGGCCAGCTGGGATCAGAG	120
Db	838991	CGGGGCGCGGAAACCGCGCATCTGTTTCGGCGCGCGCGGGGTCGGCGGCGCTCGGCGG	839050
OY	121	CAGGAGCCAGGAGCGCAGAACTGGCGCGCCCGCCCTTCCTCTGGCGCGAGGAAGCT	180
Db	839051	ATTCTGGAACCGCGGGTGCACCGGCGGGGCAAGCGGGGCGCGGGGCGGGCGGGCTGTT	839110
OY	181	CCCTCACGAGAGGAAGCTCCCTCAACCGGCG---CAGCCCTGACAGGGGGCGCGTGG	240
Db	839111	TGGCGCGGAAAGGAACCGCGCAGCGGGGTGGGCACTCACTGGCGGGGCGCGCGG	839170
OY	238	GTCAGACCGCAAAAGCAAGTGGCGGGCGGGGATGGGCTCGCGGAGCAAAAGCGCGGCGC	297
Db	839171	GCGCGCGGCAACCGCGGACACTGCGCAGCTGTGTATGGCGGGGCGCGCGGACCGCGG	839230
OY	298	TGCGCTCTCAAGAGGCGCCCAAGCGCTGCGCCCAAGAGAACTCTGAGAGCCCGGCAAGGA	357
Db	839231	CGCTAATCGAAGCGCGGATTTGGGCGGGGCGCGCGAGCGCGGCGACATCGGCACTTT	839290
OY	358	AGGAGGCAACGGGCTTCCAGAGCCCGCGCGCCCGCAGCAGAAATTGGCCAGGG-CATGGC	416
Db	839291	CTTTCGGCTCCGGCGGCTCGGGGGGCGCGCGGCAATTGTAAAGCGTGGGAGCAACGCG	839350
OY	417	CGTGAAGGAGCGGGGCGAGGGGCTTTT-----TCAGAGCGCGGGGCGAGGCGCGCGCTGG	469
Db	839351	CGCGGGGCGGGGCGGGGCGGGGCGCCCGGGGCTATCGGCAACGGCGGCAACGGCGGCAACGG	839410
OY	470	AGGAGCGAGACCGG	484
Db	839411	CGGCGGAGACCGG	839425

## RESULT 6

US-08-22-463-14/c  
Sequence 14, Application US//0822463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHERFLINGER, F.  
APPLICANT: FALKNER, P. G.  
TITLE OF INVENTION: RECOMBINANT FOMLP0X VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria

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STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TRILEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-F15
US-08-232-463-14

Query Match      8.4%; Score 47.2; DB 1; Length 7218;
Best Local Similarity 4.4%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 13; Conservative 171; Mismatches 114;

QY 223 AGGGGGGCGCTGGGTGACAGCCGAAAGAGGTGCGGGCGGGCTGCGCGGA 282
DB 1339 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
QY 283 GACAAAGCGCGGCTGCTCTCTCAGAGGCGCCGCGGCTGCCAAGAGAGTCTCG 342
DB 1279 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
QY 343 AGCGCGCGGAGGAGGCGGCGGCTTCCAGAGCGCGCGCGCGCGAGGAAATT 402
DB 1219 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
QY 403 GGCGAGGCGAGCGCGTGAAGAGGCGGCGGCTTCTCAGAGCGCGGCGAGCGCG 462
DB 1159 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
QY 463 GGCGTGAAGGAGGAGGCGGAGGCGGTTAAAGAGCTGTTGCTTCCCGGAGCGCG 520
DB 1099 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
RESULT 7
US-08-458-912-1/c
Sequence 1, Application US/08458912
Patent No. 5650310
GENERAL INFORMATION:
APPLICANT: Broer, Inge
APPLICANT: Hillemann, Doris
APPLICANT: Publer, Alfred
APPLICANT: Wohleben, Wolfgang
APPLICANT: Donn, Gunter
APPLICANT: Mullner, Hubert
APPLICANT: Bartsch, Klaus
TITLE OF INVENTION: DEACTYLASE GENES FOR THE PRODUCTION OF

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TITLE OF INVENTION: PHOSPHINOTHRICIN OR
TITLE OF INVENTION: PHOSPHINOTHRICYL-ALANYL-ALANINE, AND THEIR USE
TITLE OF INVENTION: PROCESSES FOR THEIR ISOLATION, AND THEIR USE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William F. Lawrence
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,912
FILING DATE: 02-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,498
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, William F.
REGISTRATION NUMBER: 28,029
REFERENCE/DOCKET NUMBER: 514410-2882
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-0712
TELEFAX: (212) 840-3333
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 932 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-458-912-1

Query Match      8.3%; Score 46.6; DB 1; Length 932;
Best Local Similarity 48.5%; Pred. No. 0.17;
Matches 164; Conservative 0; Mismatches 165; Indels 9; Gaps 1;

QY 184 TCACCGGAGGAGAGTCCCTCACCGGCGCGGCTTGCAGAGGAGGCGCGTGGGTGAGA 243
DB 744 TCGTGTACAGAGACTTCTCGGAACCGACTGTGATGACAGGAGGCGGACGCGTCAGA 685
QY 244 CCGCAAGGAGAGTGGCGGCGCGGTGGGCTGCGGAGCAAGGCGGCGCTGCTC 303
DB 684 TCGCGTGGCGGCGGAGCGGCGGAGGCGGCTTCTGAGATCGTGGCGGCGGAGTACGCGCC 625
QY 304 TCTCAGAGGCGGCGGCGGCTTCTCAGAGGAGTCTTGAAGCGGCGGCGGAGAGGAGG 363
DB 624 GCGATGCGGAGAGTCTTCTGATGTCAGAGATCTGCGCTCTTGGGGTGAAGTGC 565
QY 364 CACGGGCTTCCAGAGGCGGCGGCGGCGGCGGCGGAGGAAATTGGCCAGGCGGCGGTAAGC 423
DB 564 GAGGCGGCTTCTGAGGCGGAGTGGCGGCGGCGGCGGAGATGACACCGCGGCGGCGGAGC 505
QY 424 GGAG-----CGGCGAGGCGCTTCTCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGAG 474
DB 504 GGGTCCCGCGCGTGGCGGAGCACTTGAAGGCGGCGGAGGCGGCGGCGGCGGCGGAG 445
QY 475 CGAGAGCGGAGTAAAGAGCTGTGAGCTTGGCCCGG 512
DB 444 TCACCGGAGAGGTGATCCGCGCGGCGGAGGCGCGG 407
RESULT 8
US-08-461-179-1/c
Sequence 1, Application US/08461179
Patent No. 5668297
GENERAL INFORMATION:

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Fri Nov 7 08:48:28 2003

us-10-081-817a-19-plus-1-12-of-seq3.rn1

Page 8

QY 327 CAGAGGAGTCTCGAGCCCGGCGAG--GAGAGGGGCAAGGCGCTTCCAGGCGCG 384  
Db 335 TTCCGGGAGGCGCTCTGCGCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 276  
QY 385 CGGCGGCAAGAGTTGGCCAGGCGACGCGCGCTGAGCGGAGCGGCGCGCTTCTCA 444  
Db 275 TGTCCCGGGGCGACGACGACGAGAGGAGCGCGCGCGCTGACGACGAGCA 216  
QY 445 GAGCGCGGCGGAGCGCGCGCGCTGAGGCGGAGACCGGCTAAGAGAGCTCTGCGGC 504  
Db 215 GCGTCTGCGAGCGCCGAGGCGAGCGCGCTGCTATGTTGCGGCGCCCGCGCGCGCG 156  
QY 505 TTGCGCGGCGAGCGCGAGGTTCCCGCGCGCGCGCGAG 541  
Db 155 CTGCGGCGGCGAGCTCAATGCGCCCGGAGCGCGCG 119

RESULT 12

US-08-814-095-7

Sequence 7, Application US/08814095

Patent No. 6025183

GENERAL INFORMATION:

APPLICANT: Soreq, Hermona

APPLICANT: Zakut, Haim

APPLICANT: Shani, Moshe

TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR

TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: KOHN & ASSOCIATES

STREET: 30500 No. 6025183thwestern Highway, Suite 410

CITY: Farmington Hills

STATE: Michigan

COUNTRY: U.S.

ZIP: 48334

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/814,095

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Montgomery, Irene N.

REGISTRATION NUMBER: 38,972

REFERENCE/DOCKET NUMBER: 2391.00066

TELECOMMUNICATION INFORMATION:

TELEPHONE: (248) 539-5050

TELEFAX: (248) 539-5050

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 35060 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLCULE TYPE: other nucleic acid

DESCRIPTION: /desc = "Cosmid including ACHÉ

HYPOHETICAL: promoter, ACHÉ gene and Ars gene"

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

POSITION IN GENOME:

CHROMOSOME/SEGMENT: 7q22

FEATURE:

NAME/KEY: promoter

LOCATION: 4089..22464

OTHER INFORMATION: /function= "ACHÉ Promotor"

OTHER INFORMATION: /standard\_name= "ACHÉ Promotor"

FEATURE:

NAME/KEY: exon

LOCATION: complement (33297..33408)

LOCATION: 22465..22537  
OTHER INFORMATION: /function= "non-translated"  
OTHER INFORMATION: /gene= "ACHÉ"  
OTHER INFORMATION: /number= 1  
FEATURE:  
NAME/KEY: exon  
LOCATION: 24090..25177  
IDENTIFICATION METHOD: experimental  
OTHER INFORMATION: /function= "(translation start:  
OTHER INFORMATION: 24110)"  
OTHER INFORMATION: /evidence= EXPERIMENTAL  
OTHER INFORMATION: /gene= "ACHÉ"  
OTHER INFORMATION: /number= 2  
FEATURE:  
NAME/KEY: exon  
LOCATION: 25524..26009  
IDENTIFICATION METHOD: experimental  
OTHER INFORMATION: /evidence= EXPERIMENTAL  
OTHER INFORMATION: /gene= "ACHÉ"  
OTHER INFORMATION: /number= 3  
FEATURE:  
NAME/KEY: exon  
LOCATION: 27005..27274  
IDENTIFICATION METHOD: experimental  
OTHER INFORMATION: /evidence= EXPERIMENTAL  
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LOCATION: 27255..28007  
IDENTIFICATION METHOD: experimental  
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FEATURE:  
NAME/KEY: terminator  
LOCATION: 27385..27387  
FEATURE:  
NAME/KEY: exon  
LOCATION: 28008..28129  
IDENTIFICATION METHOD: experimental  
OTHER INFORMATION: /evidence= EXPERIMENTAL  
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OTHER INFORMATION: /number= 6  
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LOCATION: 28129..28131  
FEATURE:  
NAME/KEY: complement (34528..34895)  
LOCATION: complement (34528..34895)  
OTHER INFORMATION: /function= "arsenite resistance  
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FEATURE:  
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LOCATION: complement (33779..33963)  
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OTHER INFORMATION: /number= 3  
FEATURE:  
NAME/KEY: exon  
LOCATION: complement (33493..33591)  
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FEATURE:  
NAME/KEY: exon  
LOCATION: complement (33297..33408)  
OTHER INFORMATION: /gene= "AR"

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NAME/KEY:	exon		
LOCATION:	complement (32959..33094)		
OTHER INFORMATION:	/gene= "AR"		
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NAME/KEY:	exon		
LOCATION:	complement (32569..32628)		
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FEATURE:			
NAME/KEY:	exon		
LOCATION:	complement (32386..32468)		
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LOCATION:	complement (30470..30626)		
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NAME/KEY:	exon		
LOCATION:	complement (30187..30274)		
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NAME/KEY:	exon		
LOCATION:	complement (29945..30073)		
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OTHER INFORMATION:	/number= 15		
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NAME/KEY:	exon		
LOCATION:	complement (29664..29856)		
OTHER INFORMATION:	/gene= "AR"		
OTHER INFORMATION:	/number= 16		
US-08-814-095-7			
Query Match	8.1%; Score 45.8; DB 3; Length 35060;		
Best Local Similarity	46.8%; Pred. No. 0.27;		
Matches 176; Conservative	0; Mismatches 198; Indels 2; Gaps 1;		
DB	151	CCCCGGCCCTGCGCCGTGGCGGCAGAGAACTCCATCAGCAACNAGGAAGTCCCTCACCCG	210
QY	28265	CGCGGTCTCTGTCAATCTCTCAGACTCGAAGCTCCCTCCCGGGTGCTTCGCCCTCTGG	28324
DB	211	GCCCAGCCTTCAGAGGGGGCGCTGGGGTCAAGCCGAAAGCGAAAGTGGGGCCGGAGT	270
QY	28325	GCTGCCAATAAATTGTTACAGCAGCAGGAGATGTGGCGACTAGGAGAACCGAGGGTGAAG	28384
DB	271	GGGCTTCGGCGAGACAAGAGCCGGCTTCCTCTCTCAGAGAGGCCAGCGCCTGCAG	330
QY	28385	CAGAAGCCGGAATTCAGGAGGCCGAGTCTATTCAGAGACCGGGCTCGAAGGCAAGAAC	28444

QY 331 AGGAAGTCTTGACAGGCGCCGGGAGAAAGGGGGCAAGGGCTTCGCCAGGGCGCGCGC 390

Db 28445 AGCGAGCTTCGAGGCGGGGCGCGAAGGCACAAGCCCTTAGCCCTCGCGGGCG 28504

QY 391 CAGCAGGAAGTTGGCCA--GGCACGCGCGGTGAGCGAGCGGGCGAGGCTTTCAGAG 448

Db 28505 GACTGTGCGCGCTCGTAATGAGAGCCCGACGACGCTAGCTGGCACGGCGAGGGAGA 28564

QY 449 CGCGGCGAGCGCGCGCTTGAGAGGGCGACGACCGGATTAGAGAGCTCGTGCC 508

Db 28565 GAGGGAGGGGAGGGAGGGAGGGGCGGGCGGGCGCGGACGACATTGTGGAGCTC 28624

QY 509 CCGGCGAGCCGAGCT 524

Db 28625 CTCGTGCTGCCGT 28640

RESULT 13  
US-08-483-533-4  
; Sequence 4, Application US/08483533  
; Patent No. 6172047  
GENERAL INFORMATION:  
APPLICANT: Roizman, Bernard  
TITLE OF INVENTION: Method for Treating Tumorigenic  
DISEASES  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/483,533  
FILING DATE: 07-MAR-95  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/419,853  
FILING DATE: 11-APR-95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/861,233  
FILING DATE: 31-MAR-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, James P.  
REGISTRATION NUMBER: 28,491  
REFERENCE/DOCKET NUMBER: 28097/32742  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 595 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-483-533-4

Query Match 8.1%; Score 45.4; DB 3; Length 595;  
Best Local Similarity 46.2%; Pred. No. 0.29; Query 1  
Matches 183; Conservative 0; Mismatches 212; Indels 1; Gaps 1

23 TGAGGCTGATCGCTCGCGCTCCACCCTCCCGGCGAGAGGCCGCCACGAGAGC 82

US-RESULT 14  
US-09-883-471A-4  
Sequence 4, Application US/09283471A  
Patent No. 6340673  
GENERAL INFORMATION:  
APPLICANT: Roizman, Bernard  
APPLICANT: Chou, Joany  
TITLE OF INVENTION: Method For Treating Tumorigenic Diseases  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago

COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Vert  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/283,471A  
FILING DATE: 04-APR-1999  
CLASSIFICATION: 514  
Prior APPLICATION DATA:  
APPLICATION NUMBER: 07/861,233  
FILING DATE: 31-MAR-1992  
Prior APPLICATION DATA:  
APPLICATION NUMBER: 08/419,853  
FILING DATE: 11-APR-1995  
Prior APPLICATION DATA:  
APPLICATION NUMBER: 08/483,533  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, James P.  
REGISTRATION NUMBER: 28,491  
REFERENCE/DOCKET NUMBER: 27373/327422A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474 6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ. ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 595 base pairs  
TYPE: nucleic acid

Query Match	8.1%	Score 45.4	DB 4	Length 595
Best Local Similarity	46.2%	Pred. NO. 0.29		
Matches 183; Conservative	0	Mismatches 212	Indels 1	Gaps 1

QY 23 TGAGGCTGATATCGCTCCCTGAGGCGCTCACTCCCGAGGGCGAGAAAGGCGCCACAGAGAC 82

Dp 50 TCAGGCCCTTCCGCTTCGCGCGCGCTGTGCTTCGCTCGCGCTACGCCAGAGCAC 10

QY 83 CCCCAGTGCAGACGTGTTCGAGGATCTGAGGATCTAGAGCAGAGGACCCAGAGACCCAGAAC 14

Dp 110 CTGCGCGCGCTCGGCGCTGGACCGCGGGCGGGAGAGGAGGCGCGAGGCCCGCCGACCC 16

QY 143 TGCGCGCGCGCGCGCGCGCGCTGCGCGCGCAGAGGAACTCTCTACCTAGAGGAACTTCCC 20

Dp 170 CCGCGACACCCCGCGACCCCGCGACCCCGCGAACCCCGCGACCCCGCGACCCCGCG 22

QY 203 CTCAACCCGCGCCGAGCCCTGAGAGGGGGCGCGTGGGCTGACACCGCAAGCGAAGAGTGGC 26

Dp 230 ACCCGCGACACCCCGCGACCCCGCGCGAGGCGCTTCTCGCCCCAGTCCGGGTGGC 28

QY 263 GCGGGGTTGGGCGCTCG-CGAGACAAAGCGCGGCTCTCTCTCTCAGAGGGCGCCAGCG 32

Dp 290 CACTGTGTGTCTGGGCTCTGGGCGCGCGCGCTGTGGCGCGCGGCTCTGTGGGCGCGGAG 34

QY 322 CTGTCCAAAGAAATCTCTGAGGCGCCGAGCAGGAAAGGGAGCAACGGCTTCCAGGGCC 38

Dp 350 CGGAGCGACCGGCGCTGGTTCGGAGCGCGGGTGGAGGAGGCCAGCGCGTATCGGCGCG 40

QY 382 CGCGCGCGCGAGCAGGAAATTGGCCAGGACACCGCC 41

Dp 410 TGCCTTGGGCGCGAGGCGCGGTGCTCGGGCGCTTGGCG 44

RESULT 15  
US-08-483-533-36  
Sequence 36, Application US/08483533  
Patent No. 6172047  
GENERAL INFORMATION:  
APPLICANT: Roizman, Bernard  
APPLICANT: Chou, Joany  
TITLE OF INVENTION: Method for Treating Tumorigenic  
TITLE OF INVENTION: Diseases  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6100 Sears Tower, 235 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,533  
FILING DATE: 07-MAR-95  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/419,853  
FILING DATE: 11-APR-95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/861,233  
FILING DATE: 31-MAR-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, James P.  
REGISTRATION NUMBER: 28,491



```

REFERENCE/DOCKET NUMBER: 28097/32742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-483-533-36

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Query Match      8.1%; Score 45.4; DB 3; Length 1327;
Best Local Similarity 46.2%; Pred. No. 0.3;
Matches 183; Conservative 0; Mismatches 212; Indels 1; Gaps 1;

QY 23 TGAAGGCTATTCGTCCTGAGCGCTCCACCTCCCAAGCGGCAAGAGCCCAAGAGAC 82
DB 491 TCAAGCCCTTCGCTTCGCGCGCTGCGCTCCGCTCGGCTCAACGAGAGCAG 550
QY 83 CCCCAATGACCCGACGTTGCAAGGATCTGGATCAGAGCAAGGACCAAGAGCCAGAGAC 142
DB 551 CTGGCTGCTGAGCTGAGCTGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 610
QY 143 TGGGCGCCCGCCCGCCCTGCTGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 202
DB 611 CCGCGACCCCGCGAGACCCCGCGAGCCCGCGAGCCCGCGAGCCCGCGAGCCCGCGAG 670
QY 203 CTCACCGGCGCCGACGCTTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 262
DB 671 ACCCGCGGACCCCGCGAGCCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 730
QY 263 GCCGGGATGAGCTCG-CGAGAGCAAGAGCGGAGCTGCTCTCTCAGAGGAGGAGGAGG 321
DB 731 CACTGTGTGTCTGGGCTCTGAGCGCGCGCTGCTGCGCGCGCTGCTGAGGAGGAGGAG 790
QY 322 CCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 381
DB 791 CGAGCGGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 850
QY 382 CGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 417
DB 851 TGGCTGAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 886

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Search completed: November 6, 2003, 16:18:18  
Job time : 75 secs





Db	6	CGAGAAAGGCGCCCAAGAGAACCCCGATGCCAGATTGACAGGCTGTGGATACAGAG	120
Qy	121	CAGGAGACAGGAGAGCCAGGAACCTGGCGCGCCCCCGCCCTGCTGCTGGCGCAGAGGAAGCT	180
Db	121	CAGGAGACAGGAGAGCCAGGAACCTGGCGCGCCCCCGCCCTGCTGCTGGCGCG--AGGAAGCT	177
Qy	181	CCCTCACGAGAGGAAGCTCCCTCAACCCGCGCCAGCCTTGACAGGAGGAGCGCTGGCGCTC	240
Db	178	CCCTCACGAGAGGAAGCTCCCTCAACCCGCGCCAGCCTTGAGAGGAGCGCGGAGCTC	236
Qy	241	AGACCGCAAGCCAAAGATGCGGAGCGGAGTGGGCTCGCGAGACAAAGGCGCGGCTGCG	300
Db	237	AGACCGCAAGCCAAAGATGCGGAGCGGAGTGGGCTCGCGAGACAAAGGCGCGGCTGCG	286
Qy	301	CTCTCTCAGAGGGCCCCAGCGCTGCGCAAGAGAAAGTCTGAGAGGCCCGGCGCAGGAGAGG	360
Db	297	CTCTCTCAGAGGGCCCCAGCGCTGCGCAAGAGAAAGTCTGAGAGGCCCGGCGCAGGAGAGG	356
Qy	361	GGGCAAGGCTTCCACAGGGCCGCGCGGCGCAGCAGAAATTGGCCAGAGGCAAGCGCCGTG	420
Db	357	GGGCAAGGCTTCCACAGGGCCGCGCGGCGCAGCAGAAATTGGCGCAGAGGCAAGCGCCGTG	416
Qy	421	AGGAGAGCGGAGCGGGCTTTCTCAGAGAGCGCGGCGAGAGCGCGCTGAGAGGCGCAGAGA	480
Db	417	AGGAGAGCGGAGCGGGCTTTCTCAGAGAGCGCGGCGAGAGCGCGCTGAGAGGCGCAGAGA	476
Qy	481	CCGGGATTAAGAGAGCTCGTAGGCTTGGCCCGGCGCAGCGCAGAGTTCCCCCGCGCGCCGGA	540
Db	477	CCGGGATTAAGAGAGCTCGTAGGCTTGGCCCGGCGCAGCGCAGAGTTCCCCCGCGCGCCGGA	536
Qy	541	GGCCCCGGCGCC	551
Db	537	GGCCCCGGCGCC	547

```

RESULT 2
US-10-059-579-120
Sequence 120. Application US/10059579
Publication No. US20030138783a1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: SUNKUMAR, Saraswati
APPLICANT: EYRON, Elia
APPLICANT: DOOLEY, William C.
APPLICANT: DAVIDSON, Nancy
APPLICANT: FACKLER, Mary Jo.
FILE OF INVENTION: ABBREVIATED METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
FILE REFERENCE: JHU1630-1
CURRENT APPLICATION NUMBER: US/10/059.579
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: US 09/771,357
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 136
SOFTWARE: PatentIn version 3.1
SEQ ID NO 120
LENGTH: 1794
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (359)..(359)
OTHER INFORMATION: n is any nucleotide
US-10-059-579-120

```

Query Match: 92.2%; Score 350.4; DB 12; Length 1794;  
 Best Local Similarity 97.9%; Pred. No. 2e-66;  
 Matches 366; Conservative 0; Mismatches 6; Indels 2; Gaps 1

Qy 190 GAGGGAAGCTCCCTCAACCCGGGCGCAAGCCCTCAGGGGGGCGCGTGGGCTTACAGCCGCA 249  
 |||||  
 Db 812 GAGGGAAGCTCCCTCAACCCGGGCGCAAGCCCTACGGGGGCGC--TGGGTATAGACCCCA 869  
 |||||  
 Qy 250 AGCGAAGGTCCGGGCGGAGGTGGGCTTCGCGAGACAAAGGCCGGGCTGCTCTTCTCAG 309  
 |||||

Db	Sequence	Score
Dp	870 AGCGAAGGTGCGGGCGCGGGGTGGGCTCGCGGACAAAGGCCGGGCTGGCTCTTCAG	92.99
Oy	310 AGGCGCCCAAGCGGCTCTCAAGAGAAAGTCTTGAAGGCCCGGGCAGGGAAGGGGCAAGGG	36.59
Dp	930 AGGGCCCCAGCGGCTCTCAAGAGAAAGTCTTGAAGGCCCGGGCAGGGAAGGGGCAAGGG	96.89
Oy	370 CTTCCCAAGGGCCCGCGGCGCAGGAGGAAGTTGGCCAGGGCAAGCGCGCTGAGCGGAGCG	42.39
Dp	990 CTTCCCAAGGGCCCGCGGCGCAGGAGGAAGTTGGCCAGGGCAAGCGCGCTGAGCGGAGCG	104.09
Oy	430 GGCAGGAGCTTCTCAGAGAACCGCGGCGAGAGCCCGGCGCTGAGAGGGGCGAGGACCGGATTA	48.89
Dp	1050 GGCAGGAGCTTCTCAGAGAACCGCGGCGAGAGCCCGGCGCTGAGAGGGGCGAGGACCGGATTA	110.09
Oy	490 AGAAGCCTCGTGCGCTTTGCGCGGAGCAGCGCAGGTTCCCGCGCGCCCGAGAGCCCGCG	54.99
Dp	1110 AGAAGCCTCGTGCGCTTTGCGCGGAGCAGCGCAGGTTCCCGCGCGCCCGAGAGCCCGCG	116.09
Oy	550 CCATGAAGCTCGCC 563	
Dp	1170 CCATGAAGCTCGCC 1183	

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RESULT 3
US-10-027-632-196114/c
; Sequence 196114, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196114
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-196114

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	Query Match	25.5%;	Score 143.6;	DB 12;	Length 533;
	Best Local Similarity	94.8%;	Pred. 10.3-7e-22;		
	Matches 181;	Conservative	0;	Mismatches 5;	Indels 3
Oy	1	CGGCGGGAGGAGGCGGCGCGGAGTGAAGGCTAGTCCCTCGGCGCCCTCCACCTCCGAG	60		
Db	189	CGGCGGGAGGAGGCGGCGGAGTGAAGGCTAGTCCCTCGGCGCCCTCCACCTCCGAG	130		
Oy	61	CGGAGAAAGCGCGCCACAGAGACCCCACTGGCCGACGTTGCGACAGTCTGGATATCAGAG	120		
Db	129	CGGAGAAAGCGCGCCACAGAGACCCCACTGGCCGACGTTGCGACAGTCTGGATCAGAG	70		
Oy	121	CA-GGGAACCAAGGAGCGCAGAACTCGCCGCCGCCGCCCTTGCCTTGGCCGAGGAAGC	179		
Db	69	CACGGAGCAAGGAGCGCAGAACTCGCGGCC--GACCTCTGCTTACGCGAGA-GGAAGC	14		

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QY 180 TCCTCACCNG 190
      |||||
      13 TCCTCACCNG 3

RESULT 4
US-10-027-632-196114/c
; Sequence 196114, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196114
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-196114

Query Match      25.5%; Score 143.6; DB 13; Length 533;
Best Local Similarity 94.8%; Pred. No. 3.7e-22;
Matches 181; Conservative 0; Mismatches 5; Indels 5; Gaps 3;

QY 1 CGGCGGAGGAGCGGCGGAGTGAAGCCTGATCGTCCCTGCGGCTTCCACCTTCCCGAG 60
DB 189 CGGCGGAGGAGCGGCGGAGTGAAGCCTGATCGTCCCTGCGGCTTCCACCTTCCCGAG 130
QY 61 CGGAGAGGAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
DB 129 CGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 70
QY 121 CA-GGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 179
DB 69 CAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG---CGCCTGCTGGGCGGA-GGAAGC 14
QY 180 TCCTCACCNG 190
      |||||
      13 TCCTCACCNG 3

RESULT 5
US-10-237-435-6
; Sequence 6, Application US/10237435.
; Publication No. US20030124580A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Spurio, Lynn E.
; APPLICANT: Muri, Peter A.
; TITLE OF INVENTION: LONG SURFACTANT MOLECULES
; FILE REFERENCE: PB-0019 US
; CURRENT APPLICATION NUMBER: US/10/237,435
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/317,822
; PRIOR FILING DATE: 09-07-2001
; NUMBER OF SEQ ID NOS: 9
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; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124580A1 242745.1
US-10-237-435-6

Query Match      22.7%; Score 128; DB 14; Length 561;
Best Local Similarity 100.0%; Pred. No. 7.6e-19;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 436 GCTTCTCAGAGCGGCGGAGGCGGCGGCTGAGAGGAGGAGCGGATATAGAGC 495
DB 1 GCTTCTCAGAGCGGCGGAGGCGGCGGCTGAGAGGAGGAGCGGATATAGAGC 60
QY 496 CTGCTGCGCTTGGCGGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 555
DB 61 CTGCTGCGCTTGGCGGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
QY 556 AGCTCGCC 563
DB 121 AGCTCGCC 128

RESULT 6
US-10-210-951-27
; Sequence 27, Application US/10210951
; Publication No. US20030170228A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Masters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Warshaw, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P293191.1
; CURRENT APPLICATION NUMBER: US/10/210,951
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/06511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; Remaining prior application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 27
; LENGTH: 569
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TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-210-951-27

Query Match  
Best Local Similarity 100.0%; Score 90; DB 12; Length 569;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 474 GCGAGACCGGGTATTAAGAGCTCTGCGCTTGCCCGGAGCGCGAGTTCCCGCGC 533  
Db 1 GCGAGACCGGGTATTAAGAGCTCTGCGCTTGCCCGGAGCGCGAGTTCCCGCGC 60

Qy 534 GCGCGAGCGCGCGCGCATGAAGCTCGCC 563  
Db 61 GCGCGAGCGCGCGCGCATGAAGCTCGCC 90

## RESULT 7

US-10-211-884-27  
Sequence 27, Application US/10211884  
Publication No. US20030175900A1  
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Marshers, Scot A.  
APPLICANT: Pan, James  
APPLICANT: Pitli, Robert M.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stone, Donna M.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR  
FILE REFERENCE: P2931R1C1  
CURRENT APPLICATION NUMBER: US/10/211,884  
CURRENT FILING DATE: 2002-08-02  
PRIOR APPLICATION NUMBER: 60/014699  
PRIOR FILING DATE: 1996-04-01  
PRIOR APPLICATION NUMBER: 60/026943  
PRIOR FILING DATE: 1996-09-23  
PRIOR APPLICATION NUMBER: 60/059121  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/062037  
PRIOR FILING DATE: 1997-10-10  
PRIOR APPLICATION NUMBER: 60/063755  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063045  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/066511  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066772  
PRIOR FILING DATE: 1997-11-24  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 258  
SEQ ID NO 27  
LENGTH: 569  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-211-884-27

Query Match  
Best Local Similarity 100.0%; Score 90; DB 12; Length 569;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 474 GCGAGACCGGGTATTAAGAGCTCTGCGCTTGCCCGGAGCGCGAGTTCCCGCGC 533  
Db 61 GCGAGACCGGGTATTAAGAGCTCTGCGCTTGCCCGGAGCGCGAGTTCCCGCGC 60

Db 1 GCGAGACCGGGTATTAAGAGCTCTGCGCTTGCCCGGAGCGCGAGTTCCCGCGC 60  
Qy 534 GCGCGAGCGCGCGCGCATGAAGCTCGCC 563  
Db 61 GCGCGAGCGCGCGCGCATGAAGCTCGCC 90

## RESULT 8

US-09-989-722-407  
Sequence 407, Application US/09989722  
Patent No. US20020072067A1  
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-02  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088026  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088028  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088029  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088030  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088033  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088326  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088167  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: 60/088202  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: 60/088212  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: 60/088217  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: 60/088655  
 PRIOR FILING DATE: 1998-06-09  
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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C62  
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/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Deonoyers, Luc
/ APPLICANT: Baton, Dan L.
/ APPLICANT: Perrazza Napoleone
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/ APPLICANT: Wood, William I.
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Patent No. US20020072497A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
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APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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Patent No. US20020103125A1
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APPLICANT: Ashkenazi, Avi J.
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APPLICANT: Zhang, Zemin
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FILE OR INVENTION: Acids Encoding the Same
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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David

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; Patent No. US2002121576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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PRIOR FILING DATE: 1998-07-09

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Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15  
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Sequence 407, Application US/09990442  
Patent No. US20020132252A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Garber, Hanspeter  
APPLICANT: Gerlitsen, Maty E.



APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavitt, Ivar J.  
APPLICANT: Nadler, Mary A.  
APPLICANT: Paoli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C8  
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Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: November 6, 2003, 17:12:32  
Job time : 217 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 13:59:01 : Search time 1933 Seconds  
(without alignments)  
7078.852 Million cell updates/sec

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Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	77.6	13.8	1203	29	CNS015Y4	AL106054 Drosophila
6	77.2	13.7	925	29	CNS0091P	AL1053013 Drosophila
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8	74.8	13.3	949	29	AG043499	AG043499 Pan trogl
9	73.6	13.1	1065	13	CNS00720	AL066474 Drosophila
10	73.6	13.1	1101	29	CNS0175Y	BG081076 AGENCOURT
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34	72.4	12.9	1085	29	AG080291	AG080291 Pan trogl
35	72.4	12.9	1085	29	AG080291	AG080291 Pan trogl
36	72.4	12.9	1085	29	AG080291	AG080291 Pan trogl
37	72.4	12.9	1085	29	AG080291	AG080291 Pan trogl
38	72.4	12.9	1085	29	AG080291	AG080291 Pan trogl
39	72.4	12.9	1085	29	AG080291	AG080291 Pan trogl
40	72.4	12.9	1085	29	AG080291	AG080291 Pan trogl
41	72.4	12.9	1085	29	AG080291	AG080291 Pan trogl
42	72.4	12.9	1085	29	AG080291	AG080291 Pan trogl
43	72.4	12.9	1085	29	AG080291	AG080291 Pan trogl
44	72.4	12.9	1085	29	AG080291	AG080291 Pan trogl
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# ALIGNMENTS

RESULT 1	BX415111/c	982 bp	mRNA	EST 15-MAY-2003
LOCUS	BX415111	Homo sapiens THYMUS	Homo sapiens	cdna clone CS0CAP004Y120
DEFINITION	5-prime. mRNA sequence.			
ACCESSION	BX415111.1	GI:30765470		
VERSION	BX415111			
KEYWORDS	EST.			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens (human)			
REFERENCE	1. (bases Gruber C., Jesse J. and Polayes D.			
AUTHORS	1. (bases Gruber C., Jesse J. and Polayes D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished			
COMMENT	Contact: Genoscope Genoscope Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID: CS0CAP004BE10Q1.			
FEATURES	source			
	1..982			
	/organism="Homo sapiens"			

BASE COUNT  
ORIGIN

177 a 257 c 323 g 18 t 207 others

[illegible]

RESULT 2	CNS006XK		935 bp	DNA	linear	GSS 03-JUN-1995			
CNS006XK									
LOCUS	Drosophila melanogaster genome survey sequence T7 end of BAC #								
DEFINITION	BACFIN09 of RCI1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.								
ACCESSION	AU066051								
VERSION	AL066051.1								
KEYWORDS	GSS.								
SOURCE	Drosophila melanogaster (fruit fly)								
ORGANISM	Drosophila melanogaster								
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;								
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;								
	Ephyroidea; Drosophilidae; Drosophila.								
REFERENCE	1 (bases 1 to 935).								
AUTHORS	Genoscope.								
TITLE	Direct Submission								
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequence BP 191 91006 EVRY cedex - FRANCE (E-mail : seqdef@genoscope.cns.fr - Web : www.genoscope.cns.fr )								
COMMENT	determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila								

melanogaster genome using these BACs. For further information please see [http://www.fruitfly.org/The\\_BDOP\\_drosophila\\_melanogaster\\_BAC\\_library](http://www.fruitfly.org/The_BDOP_drosophila_melanogaster_BAC_library) was prepared by Kazutoyo Oosawa and Aaron Mammocer in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed in *NotI*/EcoRI digestion of *Drosophila* DNA provided by the BDOP from the isogenic strain y2; cn bw sp, the same strain used for the BDOP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACpac Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

Location/Qualifiers  
1..935

BASE COUNT	257 a	170 c	162 g	96 t	250 others
ORIGIN					

	Query Match	14.4%	Score 81.2;	DB 29;	Length 935;
	Best Local Similarity	32.9%	Pred. No. 1.5e-05;		
	Matches 130;	Conservative 92;	Mismatches 173;	Indels 0;	Gaps 0
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Qy 145 CGCGCCCCCGCCCTTGCCCTTGCGCGAGGAAAGTTCCTCAACNAGAGGAAGCTCCCT 20  
Db 538 GCGGCTCCGCGSCTSCMGCCCTGCKCGGCGCCCTSCSSSSCCSBSTSTCTBCTK 59  
Qy 205 CACCGCGGCCCGCCCTGACGCGGGCGCGCTGGGTCAACCCCAAGCGAAGTCTCGGC 26  
Db 598 SAGCTGAGCTCCCGGGGSGCGCGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 65  
Qy 265 CGGGGTGGGCGCTCGCGGACAAAGCCGGGCTGCTTCTCAAGAGGCGCCCAAGCGCT 32  
Db 658 CGSSSGGGGGSGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 71  
Qy 325 GCGAAGAGAAATCTTGAGCGCCCGGCGAGGAAAGGAGCACGAGCTTCCAGGCGCCG 38  
Db 718 CScSSCGCGSGCSSSGCCSCCGSCGSSSSSCSCCGCGMSGCGSGCGC 77  
Qy 385 CGGCGGAGAGAAATTGGCCAGGCGACGCGCTGACCGGAGCGGCGAGGCTTCTCA 44  
Db 778 CGGCGCGSGCGCGSGCGCGCGCGCGSGSGGCGGCGSSSGSGSCSCSCGCGCGSC 83  
Qy 445 GAGCGGGGCGAGGCGCGCGCGCTGAGAGGGGCGAGACCGAGTATMAACCTGTGCGC 50  
Db 838 SGGCGCGSSCGCGCGSGSGSCCGSGCGGCGGCGGSGSGSGSGCGGCGSGGCG 89  
Qy 505 TTGCGCGGACCGCGAATTCCCGCGCGCGCGC 53  
Db 898 SCGCGGCG 93

RESULT 3	BX415111	982 bp	EST 15-MAY-2003
LOCUS	BX415111		
DEFINITION	BX415111 Homo sapiens THYMUS	Homo sapiens	cdNA clone CSOACPO004Y120
ACCESSION	5-PRIME	mRNA sequence.	
VERSION	BX415111		
KEYWORDS	BX415111.1	GI:30765470	
SOURCE	Homo sapiens	(human)	
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Li,W.B., Gruber,C., Jesse,J., and Polayes,D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished		
COMMENT	Contact: Genoscope		

Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID: CS0CAP004BEI00P1.

## FEATURES

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/organism="Homo sapiens"  
/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/clone="CS0CAP004Y120"  
/issue\_type="THYMUS"  
/note="Vector: PCWVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the PCWVSPORT 6 vector.  
Library was not normalized."  
BASE COUNT 177 a 257 c 323 g 18 t 207 others

## ORIGIN

Query Match 14.4%; Score 81; DB 13; Length 982;  
Best Local Similarity 32.7%; Pred. No. 1.6e-05;  
Matches 145; Conservative 97; Mismatches 202; Indels 0; Gaps 0;  
100 GCCACGCTGTGGATCAGAGCAGGAGCCAGGAGCCAGAACTGCGCCGCCGCCGCC 159  
129 SSSGAGGAGSSG 188  
160 TGCCCTGGCGCGAGGAGGAGCTCCCTCAGAGGAGGAGTCCCTCAGCGCGCCAGCC 219  
189 KCCCCCKCCCCCCCCCGGCGGCGGCCCCSSSSSSSSSSSSSSSSSSSSSSSSSS 248  
220 TGCAGGCGGCGCGCGGTGTGATCAGAGCCGCAAGAGTGTGCGGCGGCGGTGCTCCG 279  
249 CCCCCCCCCCCCCCGGCGGCGGCCCCSSSSSSSSSSSSSSSSSSSSSSSSSSG 308  
280 GGAGCAAAAGCGCGCGCTGCTCTCAGAGGCGCCCGAGCGCTCCCAAGAGAGTGC 339  
309 GCGSSCGCGGCGGSS 368  
340 TCGAGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 399  
369 CCGGSSCGGCGGCGGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 428  
400 GTTGGCGAGGAGCGCGCGCTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 459  
429 CGSSGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 488  
460 CCGGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 519  
489 GGGGCGSSCGSSGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 548  
520 CAGGTTCCCG 548  
549 GCCCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 572

RESULT 4  
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LOCUS Pan troglodytes DNA, clone: PTB-007M05.F, genomic survey sequence.  
DEFINITION AG032885  
ACCESSION AG032885  
VERSION AG032885.1 GI:16559758  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
REFERENCE 1  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,

TITLE Totoki, Y., Matanabe, H. and Sakaki, Y.  
JOURNAL BAC end sequences of library PTB  
REFERENCE 2 (bases 1 to 1313)  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
Totoki, Y., Matanabe, H. and Sakaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suicho-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: chimpansegsc.riken.go.jp, URL: http://bgp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB. This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.

## COMMENT

PRIMERS  
Sequencing: -21M13

LIBRARY Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

## FEATURES

source

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/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-007M05.F"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_id="PTB Chimpanzee Male BAC Library"  
BASE COUNT 65 a 389 c 502 g 132 t 225 others

Query Match 13.9%; Score 78; DB 29; Length 1313;  
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Matches 231; Conservative 0; Mismatches 303; Indels 0; Gaps 0;

27 GCTTATGCTCTGCGCGCTCTCACTCCGAGCGCGAGAGGCGCCACGAGAGACCC 86  
412 GCG 471  
87 AGTGCAGGAGTTGCGAGGCTGTGGATCAAGGAGGAGGAGGAGGAGGAGGAGG 146  
472 GCG 531  
147 CCG 206  
532 GCG 591  
207 CCG 266  
592 GCG 651  
267 GGTGGGCTCTGCGGAGCAAAAGCGGCGCTGCTCTTCTCAGAGGCGCCCGCT 326  
652 CCG 711  
327 CAAGAGGAGTCTTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 386  
712 CGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCGNCG 771  
387 GCCGCGAGGAGGAGTTGGCCAGGCGACCGCGCTGAGCGGAGCGGAGGCTTTCT 446  
772 CGNCGGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 831  
447 AGCGCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 506  
832 CCG 891  
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892 GNGCGNCG 945

[illegible]

	RESULT: 6
CNS0091P/c	CNS0091P
LOCUS	Drosophila melanogaster genome survey sequence 1c73 end of BAC #
DEFINITION	BACR19D6 of RPc1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL053013 GI:4934441
VERSION	GSS.
KEYWORDS	Drosophila melanogaster (fruit fly)
SOURCE ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 925) Genoscope. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ososawa and Aaron Mammoser in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPc1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPac Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
AUTHORS	location/Qualifiers
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	/clone_1BACR19D6"
	/clone_11B=RPc1-98"
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BASE COUNT	120 a 61 c 61 g 172 t 511 others
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Best Local Similarity	13.3%; Pred. No. 8.1e-05;
Matches	48; Conservative 185; Mismatches 128; Indels 0; Gaps 0;
Oy	178 GCTCCCTCACCGGAGGAAGTCCCTCCACCACGGCCAGCCTTCGACGAGGGGCGGTGG 237
Db	:::     :::     :::     :::     :::     :::     :::     :::
Oy	918 SCGCSBSBCSSSMSTSSNSBSCSSBSBSSTSSMSBSBSBSBSBSBSBSBSBSBSBS 859
Db	:::     :::     :::     :::     :::     :::     :::     :::
Oy	238 GTCCAGCGCAAGGAAAGTGCGGGCGGGGGGCGGCGCTTCGGGAGACAAGAGCCGGGCC 297
Db	:::     :::     :::     :::     :::     :::     :::     :::
Oy	858 CTKCAASSCGCCGCAABCMCMSSSSSCGSASAGVVRVASGAKRGSGSGASASH 799
Db	:::     :::     :::     :::     :::     :::     :::     :::
Oy	298 TGCCCTCTCAGAGGGCCCCAGCGCCTCCCAAAGAAGTCTCTCAGAGCCCGGCAGAGGA 357
Db	:::     :::     :::     :::     :::     :::     :::     :::
Oy	798 SSSASBSBSSSSCASASSSSSASSSSRGGAGGASBSBSBSBSBSBSBSBSBSBASGV 739
Db	:::     :::     :::     :::     :::     :::     :::     :::
Oy	358 AGGGGCAAGGCTTCCAGGGGCCCGCGGCGCGACAGAGAAATTGGCCAGGCAAGGCC 417
Db	:::     :::     :::     :::     :::     :::     :::     :::

[illegible]

FEATURES	source
1	1. .949
2	2. (bases 1 to 949)
3	3. BAC end and sequences of library PTB
4	4. Unpublished
5	5. Direct Submission
6	6. Submitted (02-AUG-2001) Aaro Fujiyama, The Institute of Physical
7	7. 1-7-22, Senriho-cho, Ibaraki-shi, Ibaraki, Japan
8	8. Te:81-45-503-9111, Fax:81-45-503-9170
9	9. Clones are derived from the chimpanzee BAC library PTB This BAC end
10	10. was generated during the R&D process and may have higher chance of
11	11. clone tracking errors.
12	12. PRIMERS
13	13. Sequencing: -21M13
14	14. LIBRARY
15	15. Vector : pKS145
16	16. R.Site 1 : SacI
17	17. R.Site 2 : SacI
18	18. Location/Qualifiers
19	19. 1. .949
20	20. 2. (bases 1 to 949)
21	21. 3. BAC end and sequences of library PTB
22	22. 4. Unpublished
23	23. 5. Direct Submission
24	24. 6. Submitted (02-AUG-2001) Aaro Fujiyama, The Institute of Physical
25	25. 1-7-22, Senriho-cho, Ibaraki-shi, Ibaraki, Japan
26	26. Te:81-45-503-9111, Fax:81-45-503-9170
27	27. Clones are derived from the chimpanzee BAC library PTB This BAC end
28	28. was generated during the R&D process and may have higher chance of
29	29. clone tracking errors.
30	30. PRIMERS
31	31. Sequencing: -21M13
32	32. LIBRARY
33	33. Vector : pKS145
34	34. R.Site 1 : SacI
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36	36. Location/Qualifiers
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38	38. 2. (bases 1 to 949)
39	39. 3. BAC end and sequences of library PTB
40	40. 4. Unpublished
41	41. 5. Direct Submission
42	42. Submitted (02-AUG-2001) Aaro Fujiyama, The Institute of Physical
43	43. 1-7-22, Senriho-cho, Ibaraki-shi, Ibaraki, Japan
44	44. Te:81-45-503-9111, Fax:81-45-503-9170
45	45. Clones are derived from the chimpanzee BAC library PTB This BAC end
46	46. was generated during the R&D process and may have higher chance of
47	47. clone tracking errors.
48	48. PRIMERS
49	49. Sequencing: -21M13
50	50. LIBRARY
51	51. Vector : pKS145
52	52. R.Site 1 : SacI
53	53. R.Site 2 : SacI
54	54. Location/Qualifiers
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56	56. 2. (bases 1 to 949)
57	57. 3. BAC end and sequences of library PTB
58	58. 4. Unpublished
59	59. 5. Direct Submission
60	60. Submitted (02-AUG-2001) Aaro Fujiyama, The Institute of Physical
61	61. 1-7-22, Senriho-cho, Ibaraki-shi, Ibaraki, Japan
62	62. Te:81-45-503-9111, Fax:81-45-503-9170
63	63. Clones are derived from the chimpanzee BAC library PTB This BAC end
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65	65. clone tracking errors.
66	66. PRIMERS
67	67. Sequencing: -21M13
68	68. LIBRARY
69	69. Vector : pKS145
70	70. R.Site 1 : SacI
71	71. R.Site 2 : SacI
72	72. Location/Qualifiers
73	73. 1. .949
74	74. 2. (bases 1 to 949)
75	75. 3. BAC end and sequences of library PTB
76	76. 4. Unpublished
77	77. 5. Direct Submission
78	78. Submitted (02-AUG-2001) Aaro Fujiyama, The Institute of Physical
79	79. 1-7-22, Senriho-cho, Ibaraki-shi, Ibaraki, Japan
80	80. Te:81-45-503-9111, Fax:81-45-503-9170
81	81. Clones are derived from the chimpanzee BAC library PTB This BAC end
82	82. was generated during the R&D process and may have higher chance of
83	83. clone tracking errors.
84	84. PRIMERS
85	85. Sequencing: -21M13
86	86. LIBRARY
87	87. Vector : pKS145
88	88. R.Site 1 : SacI
89	89. R.Site 2 : SacI
90	90. Location/Qualifiers
91	91. 1. .949
92	92. 2. (bases 1 to 949)
93	93. 3. BAC end and sequences of library PTB
94	94. 4. Unpublished
95	95. 5. Direct Submission
96	96. Submitted (02-AUG-2001) Aaro Fujiyama, The Institute of Physical
97	97. 1-7-22, Senriho-cho, Ibaraki-shi, Ibaraki, Japan
98	98. Te:81-45-503-9111, Fax:81-45-503-9170
99	99. Clones are derived from the chimpanzee BAC library PTB This BAC end
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101	101. clone tracking errors.
102	102. PRIMERS
103	103. Sequencing: -21M13
104	104. LIBRARY
105	105. Vector : pKS145
106	106. R.Site 1 : SacI
107	107. R.Site 2 : SacI
108	108. Location/Qualifiers
109	109. 1. .949
110	110. 2. (bases 1 to 949)
111	111. 3. BAC end and sequences of library PTB
112	112. 4. Unpublished
113	113. 5. Direct Submission
114	114. Submitted (02-AUG-2001) Aaro Fujiyama, The Institute of Physical
115	115. 1-7-22, Senriho-cho, Ibaraki-shi, Ibaraki, Japan
116	116. Te:81-45-503-9111, Fax:81-45-503-9170
117	117. Clones are derived from the chimpanzee BAC library PTB This BAC end
118	118. was generated during the R&D process and may have higher chance of
119	119. clone tracking errors.
120	120. PRIMERS
121	121. Sequencing: -21M13
122	122. LIBRARY
123	123. Vector : pKS145
124	124. R.Site 1 : SacI
125	125. R.Site 2 : SacI
126	126. Location/Qualifiers
127	127. 1. .949

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BASE COUNT      55 a      465 c      281 g      35 t      113 others
ORIGIN

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The BDGP is constructing a physical map of the *Drosophila* melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org>. The BACPAC Resource Center melanogaster BAC library was prepared by Kazuo Oosawa and Aaron Mammot at the Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2, cn bw sp, the same strain used for the BACPACs p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).



SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 1065)
AUTHORS	NIH-MGC <a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D.

BASE COUNT	63 a	593 c	314 g	55 t	40 others
ORIGIN					

Query Match	Similarity	13.1%	Score 73.6	Dt 13.	Length 1065;
Best Local	Similarity	45.6%	Pred. No. 0	00038:	
Matches	Conservative	250;	Mismatches	296;	Indels 2; Gaps 1

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Db	900	GGGGGGGGGGGGGGGGGGGGCGCGCGCGGGGGGGCGCGCCGACGAGCGCGGGGCGGAGGCGGNC	841
OY	62	GCAGAAGCGCCACAGAGAACCCCAAGTGCCCGCAGATTGCCAAGCTTGGATACAAGGC	121
Db	840	GGGGGGGGGGGGGGGGGGGGCGCGCCGACCGAGGGGGGCGAGGGGCGCGGCGCGCGC	781
OY	122	AGGAGCACAGGGAGCCACAGAACTGCGCGCGCCCCCGCCCTGGCCCTGGCGGAGGAAAGTCC	181
Db	780	GGGGGCGCGGGGGCGGGGGCGGGCGCGCACCAGCANNCCCGGCGGGGCGGGGGCGGGGGGG	721
OY	182	CCTCAACNAGAGGGAAGCTTCCTTCAACCGGAGCCCTTCAGAGGGGGCGCGTGGGTCA	241
Db	720	GGGNGGGCGCGGGGGCGCGCGCGCGCGCGCGGGGGGGGGGGGGGGGGGGCGCCCGCGGGGC	661
OY	242	GACCGCAAAGCCGAAGGTGCGGGGCGGGGGTGGGCTTCGCGAGAGCAAAAGGCGGAGCTTGC	301
Db	660	GCGCGAGGGGGCGCGCGCGCGGGGGGGGGGGCGCGCGGGGGGGGGCGCCCGCGGGGGGGG	601
OY	302	TCTCTCAGAGGGGCCCGCAGCGCTTGGCCAAGAGAAAGTCTCGAAGCCCGGSCAGAGGAAAGG	361
Db	600	GCG--CCGGGGGCGCGCGGGGNCAGNCGAGGGGGCGGGCGCGGCGCGGGGGGGGGGGGGG	543
OY	362	GGCAGCGGGCTTCCCAAGGGCGCGCGCGCGCACAGGAATTGGCCAGGGGSCAGGCGGTGA	421
Db	542	GGGGGGGGGGCGGGGGGGCGCGGGGGGGCGCGCGGGGNCGGGGGGGGGGGGGGGGGGGSGN	483
OY	422	GCGGAGCGGCGAGGGCTTTCTCAGAGAGCCCGGCGAGGCGCGGCTGTGAAGGGCGAGAGC	481

[illegible]

	RESULT 11
LOCUS	CNS0175Y
DEFINITION	
ACCESSION	CNS0175Y
VERSION	1
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
	1101 bp DNA linear GSS 26-JUL-1999
	BACN27108 of DrosBAC library from Drosophila melanogaster (fruit fly) genomic survey sequence.
	Alt09460 Alt09460.1 GI:5628764
	GSS.
	Drosophila melanogaster (fruit fly)
	Drosophila melanogaster
	Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 1101)
	Genoscope.
	Direct Submisson
	Submitted (23-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqret@genoscope.cns.fr - Web : www.genoscope.cns.fr) determination of this BAC-end sequence was carried out as part of i collaboration with the European Drosophila Genome Project (ENGP) - <a href="http://www.edgp.ebi.ac.uk">http://www.edgp.ebi.ac.uk</a> . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Bellaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC Project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBac11.

BASE COUNT	254 a	176 c	160 g	152 t	359 others
ORIGIN					

[illegible]

```

Db      875 SSSSVVSAASASSSSSASASMAVAAAAVAVSVSVASVSSSSSCSSSSASVAVSA 934
QY      424 GGAGCGGCGAGGCTTTCTCAGAGAGCGCGCGCGCGCTGAGAGGCGGAGACCG 483
Db      935 SVAASASVSSSSSSSVSTSSASVAVSMASVSSSASSSSVSVAVVAASAA 994
QY      484 GGTATTAAGAGCCCTCGTGGCTTTGCCCGGCGAGCGGAGGTTCCCGCGCGCCGAGCC 543
Db      995 AAAAAAASASVAVSVASVSSSSSSSSSSSSSVSVSSSSSVSVSSSS 1054
QY      544 CCC 546
Db      1055 VSV 1057

RESULT 12
Bg786331/c 1040 bp mRNA linear EST 20-MAY-2001
DEFINITION Strongylocentrotus purpuratus CDNA clone PC_0028_A2_g12_MR 5', mRNA
sequence.
ACCESSION Bg786331.1 GI:14157344
VERSION EST
KEYWORDS Strongylocentrotus purpuratus
SOURCE Strongylocentrotus purpuratus
ORGANISM Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinoidae; Echinacea; Echinoida; Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 1040)
AUTHORS Zhu,X., Mahalax,G., Illies,M.R., Cameron,R.A., Davidson,E.H. and Ettensohn,C.A.
TITLE A large scale analysis of mRNAs expressed by primary mesenchyme cells of the sea urchin embryo
JOURNAL Development 128 (13), 2615-2627 (2001)
MEDLINE 21384984
PUBMED 11493577
COMMENT Contact: Ettensohn CA
Dept. Biol. Sci.
Carnegie Mellon University
4400 Fifth Avenue, Pittsburgh, PA 15213, USA
Tel: +1 412 268 15849
Email: ettensohn@andrew.cmu.edu.

FEATURES
source
1..1040
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="PC_0028_A2_g12_MR"
/tissue_type="embryo"
/cell_type="primary mesenchyme cells"
/lab_host="E.coli"
/clone_lib="Sea urchin primary mesenchyme cell cDNA library"
/note="Vector: pSPORT1, Site_1: NotI, Site_2: SalI; oligo dt priming from poly A+ RNA, directionally cloned"
BASE COUNT 20 a 499 c 472 g 44 t 5 others

Query Match 13.0%; Score 73.2; DB 12; Length 1040;
Best Local Similarity 46.9%; Pred. No. 0.00044;
Matches 259; Conservative 0; Mismatches 290; Indels 3; Gaps 1;

```

```

Db      752 GGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 693
QY      187 CCGAGAGGAAGCTCCCTCACCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 246
Db      692 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 633
QY      247 CAAAGGAGAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 306
Db      632 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 573
QY      307 CAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 366
Db      572 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 513
QY      367 GGGCTTCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 426
Db      512 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 453
QY      427 GCGGCGAGGCTTTCTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 486
Db      452 GCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 394
QY      487 ATAGAAGCCTGAGGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 546
Db      393 --CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 336
QY      547 GCGCGCATGAGC 558
Db      335 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 324

RESULT 13
BX405071 1201 bp mRNA linear EST 13-MAY-2003
LOCUS BX405071 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
DEFINITION clone CS0D006Y06 3-PRIME, mRNA sequence.
ACCESSION BX405071
VERSION BX405071
KEYWORDS BX405071.1 GI:30648111
SOURCE EST
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Poljates,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10245.r For more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0AG006BD03NP1&cluster=10245.r. Contact : Feng Liang Email : fliang@life.techn.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Paraday Avenue Genoscope sequence ID : CS0AG006BD03NP1.

FEATURES
source
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D006Y06"
/tissue_type="B CELLS (RAMOS CELL LINE)"
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pCMVSPORT_6, 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

```

BASE COUNT 62 a 448 c 462 g 5 t 224 others  
 ORIGIN  
 Query Match 12.9%; Score 72.6; DB 13; Length 1201;  
 Best Local Similarity 35.4%; Pred. No. 0.00058;  
 Matches 196; Conservative 87; Mismatches 268; Indels 3; Gaps 1;

1 CGGCGCGGAGGAGCGCGGAGTGAAGCTGATGTCCTCCGCTCCACCTCCGACG 60  
 555 MGCG 614  
 61 CGGAGAGAGCG 120  
 615 CGACCG 674  
 121 CAGGAGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 177  
 675 SGCCTCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 734  
 178 GCTCCTCTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 237  
 735 CG 794  
 238 GTCAGACCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 297  
 795 GSGCG 854  
 298 TGCCTCTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 357  
 855 CGSGCTGCG 914  
 358 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 417  
 915 GSCAGAGCG 974  
 418 GTAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 477  
 975 GCG 1034  
 478 GAGCGCGGATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 537  
 1035 MGCG 1094  
 538 CGAGCG 1094  
 1095 CCBACAVCAMGCC 1108

RESULT 14  
 AG080291/c 937 bp DNA linear GSS 03-NOV-2001  
 LOCUS AG080291/c  
 DEFINITION Pan troglodytes DNA, clone: PTB-076G14.F, genomic survey sequence.  
 ACCESSION AG080291  
 VERSION AG080291.1 GI:16632093  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
 TITLE Totsuki, Y., Watanabe, H., and Sakaki, Y.  
 JOURNAL BAC end sequences of Library PTB  
 REFERENCE 2 (bases 1 to 937)  
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
 TITLE Totsuki, Y., Watanabe, H., and Sakaki, Y.  
 JOURNAL Direct Submission  
 SUBMITTED 02-AUG-2001 Asao Fujiyama, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan  
 1-7-22 Suenho-chou, Tsukuba, Ibaraki, 305-8565, Japan  
 E-mail: chimpanzee@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/  
 Tel: 81-45-503-9111, Fax: 81-45-503-9170

COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end  
 was generated during the RAD process and may have higher chance of  
 clone tracking errors.  
 PRIMERS  
 Sequencing: -21M13  
 LIBRARY Vector : pKS145  
 R Site 1 : SacI  
 R Site 2 : SacI  
 Location/Qualifiers  
 1. 937  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 /clone="PTB-076G14.F"  
 /sex="male"  
 /cell\_type="lymphoblast"  
 /clone\_lib="PTB Chimpanzee Male BAC library"  
 BASE COUNT 28 a 414 c 454 g 24 t 17 others  
 ORIGIN  
 Query Match 12.9%; Score 72.4; DB 29; Length 937;  
 Best Local Similarity 46.5%; Pred. No. 0.00062;  
 Matches 261; Conservative 0; Mismatches 296; Indels 4; Gaps 1;

6 GGGAGGCGCGCGGAGTGAAGGCTGATGTCCTGCGGCTTCACCTCCGACGCGAG 65  
 868 GTGGGGGGGCG 809  
 66 AAGGCG 125  
 808 GCGGCG 749  
 126 ACCGAGGAGCGAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 185  
 748 CCG 689  
 186 ACNAGAGGAACTCTCTCAACCGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGG 245  
 688 GTCCCG 629  
 246 GCAGAGCGAGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 305  
 628 CG 569  
 306 TCAGAGG----GCCCGAGCGCTTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGG 361  
 568 CG 509  
 362 GCGAGCGGCTTCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 421  
 508 GGGGCG 449  
 422 GCGAGCGGCGGAGGCTTTCAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 481  
 448 GCG 389  
 482 CGGAGTAAAGAGCTGTGCGCTTCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 541  
 388 CCG 329  
 542 CCG 562  
 328 GCG 308

RESULT 15  
 AG152796 1085 bp DNA linear GSS 09-JAN-2002  
 LOCUS AG152796  
 DEFINITION Pan troglodytes DNA, clone: RP43-016F02.TJ, genomic survey  
 sequence.  
 ACCESSION AG152796  
 VERSION AG152796.1 GI:16682474

Fri Nov 7 08:48:35 2003

us-10-081-817a-19-plus-1-12-of-seq3.rst

Page 10

KEYWORDS	GSS.
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE	1
AUTHORS	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Tokoki, Y., Watanabe, H., and Sakaki, Y.
TITLE	BAC end sequences of library RFL-43
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1085)
AUTHORS	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Tokoki, Y., Watanabe, H., and Sakaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (02-AUG-2001) Asao, Fujiyama, The Institute of Physical

COMMENT Clones are derived from the chimpanzee BAC library RC1-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

```

FEATURES
  source
    library Sequencing: 100
    Vector      : PACB3.6
    R.Site 1    : ECORI
    R.Site 2    : ECORI
    Location/Qualifiers
      1..1085.

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BASE COUNT      45 a      45 c      46 g      31 t
ORIGIN
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/seq_xref="GenBank:9526"
/seq_xref="RefSeq:01602.1"
/sex="male"
/cell_type="lymphocytes"
/collection="RPCI-43 Chimpanzee Male BAC Library"

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Query Match Similarity	12.9%	Score 72.4	DB 29	Length 1085
Best Local Similarity	44.9%	Pred 0.00062		
Matches 226, Conservative	0	Mismatches 277		Indels 0; Gaps 0

[illegible][illegible]

Search completed: November 6, 2003, 16:16:47  
Job time : 1938 secs



JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Unpublished  
2 (bases 1 to 127488)  
DOE Joint Genome Institute.  
Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
On Apr 20, 2001 this sequence version replaced gi:7711676.  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>

Project Information  
Center Project Name: 78060  
Center clone name: CIT978SKB\_36B8

-----  
Summary Statistics  
Consensus quality: 110477 bases at least Q40  
Consensus quality: 117221 bases at least Q30  
Consensus quality: 120225 bases at least Q20  
Estimated insert size: 131000; pulse-field gel estimation  
Estimated insert size: 126288; sum-of-coverage estimation  
Quality coverage: 7.48 in Q20 bases; pulse-field gel estimation  
Quality coverage: 7.76 in Q20 bases; sum-of-coverage estimation.  
NOTE: This is a 'working draft' sequence. It currently  
\* consists of 13 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1  
1117 1116: contig of 1116 bp in length  
1217 1216: gap of unknown length  
1217 1216: contig of 1038 bp in length  
2255 2254: gap of unknown length  
3355 3354: contig of 1058 bp in length  
3413 3412: gap of unknown length  
3513 3512: contig of 1493 bp in length  
5006 5105: gap of unknown length  
5106 5105: contig of 2542 bp in length  
7647 7647: gap of unknown length  
7648 7747: gap of unknown length  
7748 10237: contig of 2490 bp in length  
10238 10237: gap of unknown length  
10338 10337: contig of 2103 bp in length  
12441 12440: gap of unknown length  
12541 12540: gap of unknown length  
15935 15935: contig of 3385 bp in length  
15936 16035: gap of unknown length  
16036 24396: contig of 8361 bp in length  
24397 24396: gap of unknown length  
34088 34088: contig of 14589 bp in length  
34088 34088: gap of unknown length  
34088 34088: contig of 21360 bp in length  
34088 60545: gap of unknown length  
60546 60545: contig of 18845 bp in length  
79491 79490: gap of unknown length  
79491 127488: contig of 47898 bp in length.

FEATURES  
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1. 127488

Location/Qualifiers  
1. 127488  
/organism="Homo sapiens"  
/mol\_type="Genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="5"  
/clone\_lib="CalTech human BAC library B"  
/clone\_id="CTB-36B8"

BASE COUNT  
31643 a 32392 c 31616 g 30626 t 1211 others

Query Match  
Best Local Similarity 79.6%; Score 200.6; DB 2; Length 127488;  
Matches 230; Conservative 0; Mismatches 5; Indels 17; Gaps 1;

1 CGGCCGGGAGGCGCGGAGTGAAGGCTATCGTCCCTGGCGCTCCACCTCCACAGG 60

Db 84291 CGGCCGGGAGGCGCGGAGTGAAGGCTATCGTCCCTGGCGCTCCACCTCCACAGG 84232  
Qy 61 CGCGAAGAGGCGCCACAGAGACCCCGAGTCCCGAGCTTGGCCAGGTTGGATCGAGG 120  
Db 84231 CGCGAAGAGGCGCCACAGAGACCCCGAGTCCCGAGCTTGGCCAGGTTGGATCGAGG 84172  
Qy 121 CAGGAGCAGGAGGCGCGAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
Db 84171 CAGGAGCAGGAGGCGCGAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 84112  
Qy 181 CCGTCACGAGGAGGAGGAGTCCCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
Db 84111 CCGCTTAC-----CGGAGCCAGCCCTGCAAGGAGGCGCGCGCGGTC 84069  
Qy 241 AGACCGCAAGC 252  
Db 84068 AGACCGCAAGC 84057

RESULT 2  
AC108083/c 130129 bp DNA linear HTG 25-JAN-2002  
LOCUS Homo sapiens chromosome 5 clone CTD-2013L15, WORKING DRAFT  
DEFINITION  
SEQUENCE, 4 unordered pieces.  
AC108083  
AC108083.1 GI:18369929  
HTG; HTGS PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 130129)  
DOE Joint Genome Institute.  
Unpublished  
2 (bases 1 to 130129)  
DOE Joint Genome Institute.  
Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>

Project Information  
Center Project Name: 632820  
Center clone name: CITB-HI\_2013L15

-----  
Summary Statistics  
Consensus quality: 124488 bases at least Q40  
Consensus quality: 128031 bases at least Q30  
Consensus quality: 128842 bases at least Q20  
Estimated insert size: 135000; agarose-gel estimation  
Estimated insert size: 129829; sum-of-coverage estimation  
Quality coverage: 7.97 in Q20 bases; agarose-gel estimation  
Quality coverage: 7.66 in Q20 bases; sum-of-coverage estimation.  
NOTE: This is a 'working draft' sequence. It currently  
\* consists of 4 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1  
4321 4320: contig of 4320 bp in length  
4420 4420: gap of unknown length  
23712 23712: contig of 19292 bp in length  
23812 23812: gap of unknown length  
23813 23813: contig of 24790 bp in length  
48602 48602: contig of 24790 bp in length  
48702 48702: gap of unknown length  
130129 130129: contig of 81427 bp in length.

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FEATURES
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      /chromosome="5"
      /clone_id="C1D-2013J15"
      /clone_lib="Caltech human BAC library D"
      /clone_1bp="30949 g 31146 t 300 others"
BASE COUNT      35337 a 32397 c 30949 g 31146 t
ORIGIN

Query Match      78.6%; Score 198; DB 2; Length 130129;
Best Local Similarity 90.9%; Pred. No. 9.6e-28;
Matches 229; Conservative 0; Mismatches 5; Indels 18; Gaps 1;

QY 1 CGGCGGGGAGAGCGGCGGAGTGTGAGGCTGTATGCTGCTGCGGCTGCACTCCACAG 60
DB CGGCGGGGAGAGCGGCGGAGTGTGAGGCTGTATGCTGCTGCGGCTGCACTCCACAG 24510
QY 61 CGGAGAGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB CGGAGAGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 24450
QY 121 CAGGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 180
DB CAGGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 24449
QY 181 CCTCACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 240
DB CCTCACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 24389
QY 241 AGACCGCAAGC 252
DB 24347 AGACCGCAAGC 24336

RESULT 3
LOCUS      AC106813      166777 bp      DNA      linear      HTG 07-MAR-2002
DEFINITION Homo sapiens chromosome 5 clone RP11-566L9, WORKING DRAFT SEQUENCE,
ACCESSION  AC106813      3      GI:19224876
VERSION     AC106813.3
KEYWORDS    HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVERIN.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1. (bases 1 to 166777)
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL     DOE Joint Genome Institute.
REFERENCE   2. (bases 1 to 166777)
AUTHORS     Unpublished
TITLE       Sequencing of Human Chromosome 5
JOURNAL     DOE Joint Genome Institute.
REFERENCE   3. (bases 1 to 166777)
AUTHORS     Direct Submission
TITLE       Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint
JOURNAL     Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   4. (bases 1 to 166777)
AUTHORS     Direct Submission
TITLE       Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
JOURNAL     Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT     On Mar 7, 2002 this sequence version replaced gi:18369924.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1519801
Center clone name: RP11-11366L9
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Summary Statistics

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Consensus quality: 163497 bases at least Q40
Consensus quality: 166071 bases at least Q30
Consensus quality: 166432 bases at least Q20
Estimated insert size: 166250; agarose-fp estimation
Estimated insert size: 166577; sum-of-contigs estimation
Quality coverage: 9.4 in Q20 bases; agarose-fp estimation
Quality coverage: 10.51 in Q20 bases; sum-of-contigs estimation
NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the sizes
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 62238 62337: contig of 62237 bp in length
62238 75837: gap of unknown length
75838 75937: contig of 13500 bp in length
75938 166777: gap of unknown length
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Best Local Similarity 90.9%; Pred. No. 8.9e-28;
Matches 229; Conservative 0; Mismatches 5; Indels 18; Gaps 1;

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DB CGGCGGGGAGAGCGGCGGAGTGTGAGGCTGTATGCTGCTGCGGCTGCACTCCACAG 119104
QY 61 CGGAGAGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB CGGAGAGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 119164
QY 121 CAGGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 180
DB CAGGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 119224
QY 181 CCTCACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 240
DB CCTCACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 119284
QY 241 AGACCGCAAGC 252
DB 119326 AGACCGCAAGC 119337

RESULT 4
LOCUS      AC025336/c      168347 bp      DNA      linear      HTG 25-MAR-2000
DEFINITION Homo sapiens chromosome 5 clone RP11-451H23 map 5, WORKING DRAFT
ACCESSION  AC025336      32      unorderd pieces.
VERSION     AC025336.2      GI:7328761
KEYWORDS    HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1. (bases 1 to 168347)
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL     Birren, B., Linton, L., Nusbaum, C. and Lander, E.
          Homo sapiens chromosome 5, clone RP11-451H23
          Unpublished

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Query Match 78.6%; Score 198; DB 2; Length 168347;

Best Local Similarity 90.9%; Pred. No. 8.9e-28; Mismatches 5; Indels 18; Gaps 1;

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Matches 229; Conservative 0; Mismatches 5; Indels 18; Gaps 1;
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DB 145142 CGGAGAGGCGCGCGCGGAGTGAAGGCTGATGCTCCCTGCGGCGCTCCCACTCCCAAG 145083
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DB 145082 CAGGAGCAGGAGGAGCAGGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGAACT 145023
QY 181 CCTCAGCAGGAGGAGGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGAACT 240
DB 145022 CCTCAGCAGGAGGAGGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGAACT 144981
QY 241 AGACCGCAAGC 252
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RESULT 5  
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LOCUS Homo sapiens chromosome 5 clone RP11-451H23, complete sequence.  
DEFINITION AC122714  
ACCESSION AC122714.2 GI:28827858  
VERSION  
KEYWORDS HTG.

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Fukuyama; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
TITLES 1 (bases 1 to 190024)
DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 190024)
DOE Joint Genome Institute.
JOURNAL Direct Submission
REFERENCE Submitted (25-MAY-2002) Production Sequencing Facility, DOE Joint
AUTHORS Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
TITLES 3 (bases 1 to 190024)
DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
REFERENCE Submitted (04-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
AUTHORS Drive, Walnut Creek, CA 94598, USA
TITLES On Mar 4, 2003 this sequence version replaced gi:212062277.
COMMENT Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.sbc.stanford.edu
Quality: Phrap Quality >=40.99.8% of Sequence;
Estimated Total Number of Errors is 0.9.
NOTE: Shatter libraries failed to verify the dinucleotide repeat
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ORIGIN

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Query Match 78.6%; Score 198; DB 9; Length 190024;

Best Local Similarity 90.9%; Pred. No. 8.6e-28; Mismatches 5; Indels 18; Gaps 1;

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QY 181 CCTCAGCAGGAGGAGGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGAACT 240
DB 81291 CCTCAGCAGGAGGAGGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGAACT 81250
QY 241 AGACCGCAAGC 252
DB 81249 AGACCGCAAGC 81238

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RESULT 6  
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LOCUS Penicillium marneffei STS, clone pm4a12.g, sequence tagged site.  
DEFINITION AL885775  
ACCESSION AL885775.1 GI:19337810  
VERSION



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DB 139643 TCGTCCCGCCTTGGCAGAAAGGGGGCGGGGACAGCCAGCGGGGCGCTCGCG 139702
QY 146 GCGGCCCCCGCCCTCGCGGCGAGGAGAGCTCCCTCACGAGGAGAGCTCCCTCG 205
DB 139703 GCGGCGCGGAGCCGAGGCGCGCCCGCGGACCCCTTACCCCGGCTCGAGGCTCGACT 139762
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RESULT 8  
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VERSION  
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ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 70097)  
2 (bases 1 to 70097)  
Unpublished  
AUTHORS  
Birken, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguski, J., Bork, A.,  
Bouckgeert, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,  
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Dewar, K., Dewar, K., Dodge, S., Domino, M., Doyle, M.,  
Fenster, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D.,  
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,

TITLE  
JOURNAL  
COMMENT

Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
Holland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,  
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Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T.M.,  
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Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zimmer, A., and  
Zody, N.

Direct Submission  
Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced by: 6978196.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L4780  
Center clone name: 28\_L\_5

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\* NOTE: This record contains 81 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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QY 4 CCGGAGAGGCGCGCGAGTGTGATGTCCTGCGCCCTCCCACTCCCGAGCGC 63
DB 69065 CCGGAGAGGCGCGCGAGTGTGATGTCCTGCGCCCTCCCACTCCCGAGCGC 69006
QY 64 AGAAGAGCGCGCGAGGAGTGTGATGTCCTGCGCCCTCCCACTCCCGAGCGC 123
DB 69005 TCGCGCGCGCGCGAGTGTGATGTCCTGCGCCCTCCCACTCCCGAGCGC 68946
QY 124 GAGCAGAGGAGCGCGAGGAGTGTGATGTCCTGCGCCCTCCCACTCCCGAGCGC 183
DB 68945 GCGCGCGCGCGCGAGGAGTGTGATGTCCTGCGCCCTCCCACTCCCGAGCGC 68886
QY 184 TCACGAGGAGGAGTGTGATGTCCTGCGCCCTCCCACTCCCGAGCGC 229
DB 68885 CCGGAGAGGCGCGCGAGTGTGATGTCCTGCGCCCTCCCACTCCCGAGCGC 68840

```

RESULT 9  
 TMI270035 786 bp DNA linear VRT 01-SEP-2000  
 LOCUS Tetracodon nigroviridis 18S rRNA gene (partial), 5.8S rRNA gene (partial) and internal transcribed spacer 1 (ITS1), clone C0NA019AD11.  
 ACCESSION AJ270035  
 VERSION AJ270035.1 GI:6689431  
 KEYWORDS 18S ribosomal RNA; 18S rRNA gene; 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; ITS1.  
 SOURCE Tetracodon nigroviridis  
 ORGANISM Tetracodon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neuteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthomorphi; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.  
 Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 10835645  
 2  
 Roest Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C., Frazar, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A., and Weissbach, J.  
 Estimate of human gene number provided by genome-wide analysis using Tetracodon nigroviridis DNA sequence  
 Nat Genet. 25 (2), 235-238 (2000)

## REFERENCE

AUTHORS

## TITLE

JOURNAL

MEDLINE

PUBMED

10835645

2

Roest Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C., Frazar, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A., and Weissbach, J.

Characterization and repeat analysis of the compact genome of the freshwater puterfish Tetracodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

3 (bases 1 to 786)

Roest Crolius, H.

Submitted (27-SEP-1999) Roest Crolius H., Tetracodon Group, Genoscope, 2, rue Gaston Crémieux, 91057 Evry Cedex, FRANCE

The full annotated consensus sequence of the complete Tetracodon nigroviridis rRNA gene cluster is available at

http://www.genoscope.cns.fr/ (URL provided by the submitter). This sequence corresponds to position 2151-2937 of the consensus.

location/Qualifiers

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/mol\_type="genomic DNA"

/db\_xref="taxon:9883"

/clone="C0NA019AD11"

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/gene="18S rRNA"

/product="18S ribosomal RNA"

204..660

/note="Internal transcribed spacer 1, ITS1"

661..786

/gene="5.8S rRNA"

661..786

/gene="5.8S rRNA"

/product="5.8S ribosomal RNA"

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BASE COUNT 131 a

ORIGIN

Query Match

Best Local Similarity 17.7%; Score 44.6; DB 5; Length 786;

Matches 89; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

RESULT 10  
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 LOCUS Cercopithecine herpesvirus 1 US1, US2, US3, US4, US5, US6, US7, US8, US9, US10, US11, US12 genes, complete and partial cds.  
 ACCESSION AB074432  
 VERSION AB074432.1 GI:18157353  
 KEYWORDS Cercopithecine herpesvirus 1 (monkey B virus)  
 SOURCE Cercopithecine herpesvirus 1



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/db_xref="GI:18157361"
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ERKDGSEVPAPFMEPDGAPQKGNVTGLVLEAVGSGHVSFVPRVATAR
HVFPLKAPRRPEPAGTPPRPDDESGTEPATPAPPHPTIAEVAHVRGTVSLR
TQTAIPADPDVHTDVSVMPIAHDDPYMEVWVAFVDEEGEMRIYECPLYHQ
LPECRSPADPCASAVTERLAVRRIGPCRGVPPPCSDAMESRAGLGMVGHVN
LQLRDAEASGGLYCVVYNGVHVAHGVISTASKRYNAVERSPPRYRPPVEPT
PSAQTGPRPAPAPRAARLVGLGAAGVLAAGSVACVCRGARMRAKRRDLMAP
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11714..12082
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/protein_id="BAB83756.1"
/db_xref="GI:18157362"
/translation="MTRADIATPRPRIRHTGADGRPAATRGARSPDVIGVADL
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12078..12084
12206..12478
/gene="US9"
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/codon_start=1
/product="envelope phosphoprotein"
/protein_id="BAB83757.1"
/db_xref="GI:18157363"
/translation="MEPLRLADTLESLTSETSVIPLTPAQTPEAYTESDDETRADFL
VRMGQOTALRRRRQTRAVCAVLAFLVALISGGLALVCMVLR"
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complement(13105..14040)
/gene="US10"
complement(13105..14040)
/gene="US10"
/codon_start=1
/product="tegument protein"
/protein_id="BAB83758.1"
/db_xref="GI:18157364"

Query Match 17.7%; Score 44.6; DB 14; Length 14447;
Best Local Similarity 50.5%; Pred. No. 32;
Matches 107; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 26 GGCTGATCGTCCCTGGGCTCCACCTCCCGAGCGAGAGCGCCACGAGACCCC 85
DB 5484 GGCCCTGCTCCCTGGAGCGACGACCTCCCGCCCGGCGAGCGAGAGAAATGAG 5543
QY 86 CAGTGCCCGAGCTTGCCAGCGTCTGGATCAGAGGAGGAGCAAGGAGCCAGAACTGC 145
DB 5544 TCGTCCCGCGCATTCACACAGAGGGGGCGGGAGCGCGCAAGGGGGCGCGTCCGCG 5603
QY 146 GCCCGCCCGCGCTGCTGCTGGCGCGAGGAGAGCTCCCTCAGCAGAGAGCTCCCTC 205
DB 5604 GCGCGCGGAGACGAGAGCGCGCCCGCGCGACCCCTTCACCCCGCTCGAGGCTCTACT 5663
QY 206 ACCCGCGCGAGCTCGAGAGGGGGCGGGCGGTGG 237
DB 5664 CCGGCGCGCGAGCGGGGGCGGGCGGAGAG 5695

RESULT 11
AC130306/c 66558 bp DNA linear HTG 09-AUG-2002
LOCUS Homo sapiens chromosome 11 clone RP11-126H19 map 11, LOW-PHSS
DEFINITION
SEQUENCE SAMPLING.

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ACCESSION AC130306
VERSION AC130306.1
KEYWORDS HTG, HTGS PHASE0
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 66558)
AUTHORS Birren, B., Nussbaum, C., and Lander, E.
JOURNAL Homo sapiens chromosome 11, clone RP11-126H19
TITLE Unpublished
COMMENT 2 (bases 1 to 66558)
JOURNAL Birren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Baum, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B.,
Cammarata, J., Chang, J., Chazaro, B., Choepel, Y., Collimore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hago, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Landstad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrum, J., Menene, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunthang, P., Pierre, N., Raymond, C., Retta, R., Rice, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schopback, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zemdek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/BW/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
----- Project Information
Center project name: L27898
Center clone name: 126_H_19
* NOTE: This record contains 80 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be identical and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
736 735: contig of 735 bp in length
836 835: gap of 100 bp
1573 1572: contig of 737 bp in length
1673 1672: gap of 100 bp
2400 2399: contig of 727 bp in length
2500 2499: gap of 100 bp
3321 3320: contig of 721 bp in length
3321 3320: gap of 100 bp
4038 4037: contig of 717 bp in length
4138 4137: gap of 100 bp
4388 4387: contig of 744 bp in length
4882 4881: gap of 100 bp
5715 5714: contig of 733 bp in length
5815 5814: gap of 100 bp
6541 6540: contig of 727 bp in length
6642 6641: gap of 100 bp
7361 7360: contig of 720 bp in length

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* 7362 7461: gap of 100 bp
* 7462 8214: contig of 753 bp in length
* 8215 8314: gap of 100 bp
* 8315 9056: contig of 742 bp in length
* 9057 9156: gap of 100 bp
* 9157 9916: contig of 760 bp in length
* 9917 10016: gap of 100 bp
* 10017 10732: contig of 716 bp in length
* 10733 10832: gap of 100 bp
* 10833 11543: contig of 711 bp in length
* 11544 12392: contig of 748 bp in length
* 12393 12492: gap of 100 bp
* 12493 13324: contig of 722 bp in length
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* 13326 14045: contig of 721 bp in length
* 14046 14445: gap of 100 bp
* 14446 14894: contig of 743 bp in length
* 14895 14994: gap of 100 bp
* 14995 15726: contig of 732 bp in length
* 15727 15826: gap of 100 bp
* 15827 16562: contig of 736 bp in length
* 16563 16662: gap of 100 bp
* 16663 17400: contig of 738 bp in length
* 17401 17500: gap of 100 bp
* 17501 18229: contig of 723 bp in length
* 18230 18329: gap of 100 bp
* 18330 19041: contig of 712 bp in length
* 19042 19141: gap of 100 bp
* 19142 19860: contig of 719 bp in length
* 19861 19960: gap of 100 bp
* 19961 20680: contig of 720 bp in length
* 20681 20780: gap of 100 bp
* 20781 21508: contig of 728 bp in length
* 21509 21608: gap of 100 bp
* 21609 22316: contig of 708 bp in length
* 22317 22416: gap of 100 bp
* 22417 23158: contig of 742 bp in length
* 23159 23258: gap of 100 bp
* 23259 24028: contig of 770 bp in length
* 24029 24128: gap of 100 bp
* 24129 24667: contig of 733 bp in length
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* 24968 25795: contig of 728 bp in length
* 25796 26518: contig of 723 bp in length
* 26519 27359: contig of 741 bp in length
* 27360 27459: gap of 100 bp
* 27460 28200: contig of 741 bp in length
* 28201 28300: gap of 100 bp
* 28301 29009: contig of 709 bp in length
* 29010 29109: gap of 100 bp
* 29110 29843: contig of 734 bp in length
* 29844 29943: gap of 100 bp
* 29944 30683: contig of 740 bp in length
* 30684 30783: gap of 100 bp
* 30784 31517: contig of 734 bp in length
* 31518 31617: gap of 100 bp
* 31619 32351: contig of 734 bp in length
* 32352 32451: gap of 100 bp
* 32452 33177: contig of 726 bp in length
* 33178 33277: gap of 100 bp
* 33278 33992: contig of 715 bp in length
* 33993 34092: gap of 100 bp
* 34093 34819: contig of 727 bp in length
* 34820 34919: gap of 100 bp
* 34920 35336: contig of 717 bp in length
* 35337 35637: gap of 100 bp
* 35638 36449: contig of 713 bp in length
* 36450 36549: gap of 100 bp
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* 37291 37390: gap of 100 bp

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* 38130 38229: gap of 100 bp
* 38230 38962: contig of 733 bp in length
* 38963 39062: gap of 100 bp
* 39063 39798: contig of 736 bp in length
* 39799 39898: gap of 100 bp
* 39899 40608: contig of 710 bp in length
* 40609 40708: gap of 100 bp
* 40709 41454: contig of 746 bp in length
* 41455 41554: gap of 100 bp
* 41555 42312: contig of 758 bp in length
* 42313 42412: gap of 100 bp
* 42413 43160: contig of 748 bp in length
* 43161 43260: gap of 100 bp
* 43261 43996: contig of 736 bp in length
* 43997 44096: gap of 100 bp
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* 44827 44926: gap of 100 bp
* 44927 45661: contig of 735 bp in length
* 45662 45761: gap of 100 bp
* 45762 46504: contig of 743 bp in length
* 46505 46604: gap of 100 bp
* 46605 47333: contig of 729 bp in length
* 47334 47433: gap of 100 bp
* 47434 48167: contig of 734 bp in length
* 48168 48267: gap of 100 bp
* 48268 48994: contig of 727 bp in length
* 48995 49094: gap of 100 bp
* 49095 49842: contig of 748 bp in length
* 49843 49942: gap of 100 bp
* 49943 50670: contig of 728 bp in length
* 50671 50771: gap of 100 bp
* 50771 51509: contig of 739 bp in length
* 51510 51609: gap of 100 bp
* 51610 52356: contig of 747 bp in length
* 52357 52457: gap of 100 bp
* 52457 53283: contig of 727 bp in length
* 53284 53283: gap of 100 bp
* 53284 54003: contig of 720 bp in length
* 54004 54103: gap of 100 bp
* 54104 54830: contig of 727 bp in length
* 54831 54931: gap of 100 bp
* 54931 55688: contig of 735 bp in length
* 55689 55785: gap of 100 bp
* 55786 56514: contig of 729 bp in length
* 56515 56614: gap of 100 bp
* 56615 57347: contig of 733 bp in length
* 57348 57447: gap of 100 bp
* 57448 58165: contig of 718 bp in length
* 58166 58265: gap of 100 bp
* 58266 59004: contig of 739 bp in length

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Query Match 17.7%; Score 44.6; DB 2; Length 66558;  
 Best Local Similarity 49.1%; Pred. No. 20;  
 Matches 110; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

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Oy 3 GCCGGGAGGCGCGCGGAGTGAAGCCTATCTCCCTGCGCGCTCCACCTCCCGAGGG 62
Db 20553 GCCGGGAGGCGCGCGGAGTGAAGCCTATCTCCCTGCGCGCTCCACCTCCCGAGGG 20494
Oy 63 CAGAGGCGCGCGCGGAGTGAAGCCTATCTCCCTGCGCGCTCCACCTCCCGAGGG 122
Db 20493 CAGAGGCGCGCGCGGAGTGAAGCCTATCTCCCTGCGCGCTCCACCTCCCGAGGG 20434
Oy 123 GGGAGCAGGAGGAGGAGTGAAGCCTATCTCCCTGCGCGCTCCACCTCCCGAGGG 182
Db 20433 GGGAGCAGGAGGAGGAGTGAAGCCTATCTCCCTGCGCGCTCCACCTCCCGAGGG 20374
Oy 183 CTGACGAGGAGGAGTGAAGCCTATCTCCCTGCGCGCTCCACCTCCCGAGGG 226
Db 20373 CTGACGAGGAGGAGTGAAGCCTATCTCCCTGCGCGCTCCACCTCCCGAGGG 20330

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RESULT 12  
AC093712/c 133924 bp DNA linear MAM 10-OCT-2002  
LOCUS  
DEFINITION Canis familiaris clone RP81-229G11, complete sequence.  
ACCESSION AC093712  
VERSION AC093712.2 GI:17352412  
KEYWORDS  
SOURCE HTG  
ORGANISM Canis familiaris (dog)  
REFERENCE  
AUTHORS Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
1 (bases 1 to 133924)  
Ahter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,  
Blakeley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,  
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,  
Ho,S.-L., Idol,J.R., Karlins,E., Latic,P., Lee-Lin,S.-Q.,  
Legaspi,R., Maduro,Q.L., Maduro,V.B., Masiello,C., Mastrian,S.D.,  
McCluskey,J.C., McDowell,J., Pearson,R., Prasad,A., Shevchenko,Y.,  
Stantrop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W.,  
Taungson,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,  
Zhang,L.-H. and Green,E.D.  
NISC Comparative Sequencing Initiative  
Unpublished  
TITLE NISC Comparative Sequencing Initiative  
REFERENCE 2 (bases 1 to 133924)  
AUTHORS Green,E.D.  
JOURNAL Direct Submission  
Submitted (08-SEP-2001) NIH Intramural Sequencing Center, 8717  
TITL Grovemont Circle, Gaithersburg, MD 20877, USA  
3 (bases 1 to 133924)  
Green,E.D.  
JOURNAL Direct Submission  
Submitted (05-DEC-2001) NIH Intramural Sequencing Center, 8717  
TITL Grovemont Circle, Gaithersburg, MD 20877, USA  
4 (bases 1 to 133924)  
Green,E.D.  
JOURNAL Direct Submission  
Submitted (10-OCT-2002) NIH Intramural Sequencing Center, 8717  
TITL Grovemont Circle, Gaithersburg, MD 20877, USA  
On Dec 5, 2001 this sequence version replaced gi:15528874.  
COMMENT  
----- Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: http://www.nisc.nih.gov  
Contact: nisc.zoo@hgti.nih.gov  
----- Project Information  
Center project name: cia  
Center clone name: 229G11

This sequence was finished as follows unless otherwise noted:  
all regions were double-stranded, sequenced with an  
alternate chemistry, or covered by high quality data  
(i.e., phred quality >= 30); an attempt was made to resolve  
all sequencing problems, such as compressions and repeats;  
all regions were covered by at least one plasmid subclone  
or more than one M13 subclone; and the assembly was confirmed  
by restriction digest.

CLONE LENGTH: This sequence represents the entire insert of  
this clone unless otherwise noted. If there are overlapping  
clones, the overlaps are noted in the beginning and end of  
the Features section.

FEATURES  
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/clone\_1lb="RP81"  
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/note="single clone coverage"  
BASE COUNT 37717 a 30139 c 30241 g 35827 t  
ORIGIN

Query Match 17.7%; Score 44.6; DB 4; Length 133924;  
Best Local Similarity 49.2%; Pred. No. 16;  
Matches 116; Conservative 0; Mismatches 120; Indels 0; Gaps 0;  
OY 3 GCGGGGAGAGCGCGCGGAGTAGGCTGATGCTCCCTGCGCCCTCCTACCTCCCGAGGG 62  
Db 73911 GCGGGGAGAGCGCGCGGAGTAGGCTGATGCTCCCTGCGCCCGAGAGCGCTCTTCCGCGT 73852  
OY 63 CAGAGCGCGCGCGAG 122  
Db 73851 CCGCGGAGCGCGCGCGCGAG 73792  
OY 123 GGGAGCAG 182  
Db 73791 GGGAGCAG 73732  
OY 183 CTCACGAG 238  
Db 73731 CGCAGCTGAG 73676

RESULT 13  
AC134963/c 156221 bp DNA linear HTG 16-OCT-2002  
LOCUS  
DEFINITION Canis familiaris clone RP81-262L7, WORKING DRAFT SEQUENCE, 7  
ordered pieces.  
ACCESSION AC134963  
VERSION AC134963.2 GI:24022401  
KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.  
SOURCE HTG; HTGS\_PHASE2; HTGS\_DRAFT.  
ORGANISM Canis familiaris (dog)  
REFERENCE  
AUTHORS Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
1 (bases 1 to 156221)  
Ahter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,  
Benjamin,B., Blakeley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,  
Carriaga,K., Coleman,B., Dietrich,N.L., Engle,J., Granite,S.,  
Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L.,  
Idol,J.R., Karlins,E., Latic,P., Lee-Lin,S.-Q., Legaspi,R.,  
Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C., Mastrian,S.D.,  
McCluskey,J.C., McDowell,J., Pearson,R., Prasad,A., Reddix-Dugue,N., Schandler,K.,  
Schueler,M.G., Sison,C., Stantrop,S., Thomas,J.W., Thomas,P.J.,  
Touchman,J.W., Vogt,J.L., Walker,M., Wetherby,K.D., Wiggins,L.,  
Young,A., Zhang,L.-H. and Green,E.D.  
NISC Comparative Sequencing Initiative  
Unpublished  
TITLE NISC Comparative Sequencing Initiative  
REFERENCE 2 (bases 1 to 156221)  
AUTHORS Green,E.D.  
JOURNAL Direct Submission  
Submitted (03-OCT-2002) NIH Intramural Sequencing Center, 8717  
TITL Grovemont Circle, Gaithersburg, MD 20877, USA  
3 (bases 1 to 156221)  
Green,E.D.  
JOURNAL Direct Submission  
Submitted (16-OCT-2002) NIH Intramural Sequencing Center, 8717  
TITL Grovemont Circle, Gaithersburg, MD 20877, USA  
On Oct 16, 2002 this sequence version replaced gi:23477851.  
COMMENT  
----- Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: http://www.nisc.nih.gov  
Contact: nisc.zoo@hgti.nih.gov  
----- Project Information  
Center project name: dgp  
Center clone name: 262L07

The sequence data in this record represents an 'enhanced'  
version of a Phase 2 submission. Specifically, the indicated  
order and orientation of each sequence contig has been  
established using one or more of the following: read-pair  
data from individual subclones, overlaps with neighboring  
clones, alignment with available reference sequence (e.g.,

human), as/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

## Summary Statistics

Sequencing vector:	plasmid; N/A; 100% of reads
Chemistry:	Illumina; BigDye; 100% of reads
Assembly program:	Phrap; version 0.990319
Consensus quality:	154497 bases at least Q40
Consensus quality:	155075 bases at least Q30
Consensus quality:	155482 bases at least Q20
Insert size:	138000; agarose-fp
Insert size:	155621; sum-of-contigs
Quality coverage:	12.42x in Q20 bases; agarose-fp
Quality coverage:	10.94x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1	12070:	contig of 12070 bp in length
12071	12170:	gap of unknown length
12171	24433:	contig of 12262 bp in length
24440	24583:	gap of unknown length
24540	24939:	contig of 29450 bp in length
53990	54089:	gap of unknown length
54090	74569:	contig of 20480 bp in length
74570	74669:	gap of unknown length
74670	98277:	contig of 23608 bp in length
98278	98337:	gap of unknown length
98378	1331379:	contig of 34002 bp in length
132360	1334470:	gap of unknown length
132480	1552221:	contig of 23742 bp in length.

## FEATURES

	Source	1..129822 "Canis familiaris"
		/organism="Canis familiaris"
		/mol_type="genomic DNA"
		/db_xref="taxon:9615"
		/clone="RP81-262L7"
		/clone_11b="RP81"
	misc_feature	1..70328
		/note="clone overlaps with GenBank Accession Number AC093172 clone RP81-229G11 (center project name cia)"
	misc_feature	1..130710
		/note="assembly_fragment clone end:SP6 vector_side:left"
	misc_feature	12171..24439
		/note="assembly_fragment"
	misc_feature	24540..53389
		/note="assembly_fragment"
	misc_feature	54090..74569
		/note="assembly_fragment"
	misc_feature	74670..98277
		/note="assembly_fragment"
	misc_feature	98378..1132379
		/note="assembly_fragment"
	misc_feature	132480..156221
		/note="assembly_fragment missing T7 clone end from 3' end of insert"
BASE COUNT	42362 a	35542 c 35367 g 41746 t 604 others
ORIGIN		

[illegible]

RESULT 14

LOCUS	AC024956	178534 bp	DNA	linear	HTG 13-JUL-2000
DEFINITION	Homo sapiens chromosome 4 clone RPL-419B8 map 4, LOW-PASS SEQUENCING				
ACCESSION	AC024956				
VERSION	AC024956..3	GI:7328746			
KEYWORDS	HTG; HTGS - PHASED.				
SOURCE	Homo sapiens (human)				
ORANISM	Homo sapiens				

TITTLE  
JOURNAL

**JOURNAL** Submitted (03-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 25, 2000 this sequence version replaced gi:7280325.  
All features were identified using RepeatMasker.

\* NOTE: This record contains 216 individual

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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
685      684: contig of 684 bp in length
785      1479: gap of 100 bp
1480      1579: contig of 695 bp in length
1580      2281: contig of 702 bp in length
2282      2381: gap of 100 bp
3092      3091: contig of 710 bp in length
3192      3191: gap of 100 bp
3872      3871: contig of 680 bp in length
3972      3971: gap of 100 bp
4678      4677: contig of 706 bp in length
4778      4777: gap of 100 bp
5500      5499: contig of 722 bp in length
5600      6322: contig of 723 bp in length
6323      6422: gap of 100 bp
6423      7133: contig of 710 bp in length
7133      7232: gap of 100 bp
7232      7925: contig of 693 bp in length
7926      8025: gap of 100 bp
8026      8722: contig of 637 bp in length
8723      8822: gap of 100 bp
8823      9515: contig of 693 bp in length
9516      9615: gap of 100 bp
10301     10300: contig of 685 bp in length
10401     10400: gap of 100 bp
11077     11076: contig of 676 bp in length
11177     11176: gap of 100 bp
11883     11883: contig of 707 bp in length
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12709     13528: gap of 100 bp
12809     13528: contig of 720 bp in length
13529     13628: gap of 100 bp
13629     14350: contig of 722 bp in length
14351     14451: gap of 100 bp
14451     15114: contig of 664 bp in length
15115     15215: gap of 100 bp
15215     15900: contig of 686 bp in length
15901     16000: gap of 100 bp
16001     16790: contig of 690 bp in length
16791     17484: gap of 100 bp
17485     17585: contig of 694 bp in length
17586     18270: gap of 100 bp
18271     18370: contig of 686 bp in length
18371     18771: gap of 100 bp
18772     19065: contig of 695 bp in length
19066     19166: gap of 100 bp
19166     19880: contig of 715 bp in length
19881     19980: gap of 100 bp
19981     20691: contig of 711 bp in length
20692     20791: gap of 100 bp
20792     21509: contig of 718 bp in length
21510     21610: gap of 100 bp
21610     22327: contig of 717 bp in length
22327     22426: gap of 100 bp
22427     23126: contig of 700 bp in length
23127     23226: gap of 100 bp
23227     23925: contig of 699 bp in length
23926     24025: gap of 100 bp
24026     24748: contig of 723 bp in length
24749     24848: gap of 100 bp
24849     25531: contig of 683 bp in length
25531: contig of 683 bp in length

25532     25631: gap of 100 bp
25632     26330: contig of 689 bp in length
26331     26420: gap of 100 bp
26421     27110: contig of 690 bp in length
27111     27210: gap of 100 bp
27211     27913: contig of 703 bp in length
27914     28014: gap of 100 bp
28014     28723: contig of 710 bp in length
28724     28823: gap of 100 bp
28824     29544: contig of 721 bp in length
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29645     30363: contig of 719 bp in length
30364     30463: gap of 100 bp
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31933     32032: gap of 100 bp
32033     32739: contig of 707 bp in length
32740     32839: gap of 100 bp
32840     33503: contig of 664 bp in length
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33603     34294: contig of 691 bp in length
34295     34394: gap of 100 bp
34395     35091: contig of 697 bp in length
35092     35191: gap of 100 bp
35192     35906: contig of 715 bp in length
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36007     36714: contig of 708 bp in length
36715     36815: gap of 100 bp
36815     37515: contig of 701 bp in length
37516     37615: gap of 100 bp
37616     38287: contig of 672 bp in length
38288     38387: gap of 100 bp
38388     39065: contig of 678 bp in length
39066     39165: gap of 100 bp
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39857     39956: gap of 100 bp
39956     40660: contig of 704 bp in length
40661     40760: gap of 100 bp
40760     41487: contig of 727 bp in length
41488     41587: gap of 100 bp
41587     42323: contig of 736 bp in length
42324     42423: gap of 100 bp
42424     43126: contig of 703 bp in length
43127     43226: gap of 100 bp
43227     43980: contig of 754 bp in length
43981     44080: gap of 100 bp
44081     44774: contig of 694 bp in length
44775     44874: gap of 100 bp
44875     45564: contig of 690 bp in length
45565     46261: gap of 100 bp
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46362     46461: gap of 100 bp
46462     47171: contig of 710 bp in length
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47962     48061: gap of 100 bp
48062     48776: contig of 715 bp in length
48777     48877: gap of 100 bp
48877     49578: contig of 702 bp in length
49579     49678: gap of 100 bp
49679     50385: contig of 707 bp in length
50386     50485: gap of 100 bp
50486     51192: contig of 707 bp in length
51193     51292: gap of 100 bp
51293     51984: contig of 692 bp in length
51985     52085: gap of 100 bp
52085     52786: contig of 702 bp in length
52787     52886: gap of 100 bp
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* 54474 55152: contig of 679 bp in length
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Best Local Similarity 49.8%; Pred. No. 16; Mismatches 112; Indels 0; Gaps 0;
Matches 111; Conservative 0;

QY 20 GAGTGGAGCCCTGATGTCCTCCGCGCCCTCCACCTCCCGAGCGCGAGAGGCGCCCGACAG 79
DB 141570 GAGTGGATCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 141629
QY 80 GACCCCGACGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 139
DB 141630 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 141689
QY 140 AACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 199
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RESULT 15
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LOCUS Homo sapiens chromosome 8 clone RP11-314C19 map 8, LOW-PASS
DEFINITION SEQUENCE SAMPLING.
ACCESSION AC084084.2 GI:13446278
VERSION AC084084.2
KEYWORDS HTG; PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 71032)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
JOURNAL Homo sapiens chromosome 8, clone RP11-314C19.
REFERENCE 2 (bases 1 to 71032)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavsky, L.,
Bouhagalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, P.,
Choquet, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Deaellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P.,
Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,
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Lamaszates, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G.,
Macdonald, P., Margolis, N., McCarthy, M., McEwan, P., McKernan, K.,
McPherson, R., Melidim, J., Meneis, L., Mihova, T., Miener, A.,
O'Donnel, P., O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K.,
Pierre, N., Pisan, C., Pollara, V., Raymond, C., Rieback, M., Riley, R.,
Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,
Souza, N., Spencer, B., Stange-Thumann, N., Stojanovic, N., Theodore, J.,
Straus, N., Sudhakar, A., Tajamas, J., Testa, S., Theodor, J.,
Tirrell, A., Travers, M., Trifilio, V., Vassiliev, H., Vial, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W.D., Young, G., Zainoun, J.,
Zimmer, A. and Zody, M.
DIRECT SUBMISSION
Submitted (12-OCT-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 25, 2001 this sequence version replaced gi:10799449.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information

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Center project name: L11327
Center clone name: 314_C19
NOTE: This record contains 85 individual
sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
1 720: contig of 720 bp in length
721 820: gap of 100 bp
821 1257: contig of 737 bp in length
1258 1657: gap of 100 bp
1658 2404: contig of 747 bp in length
2405 2504: gap of 100 bp
2505 3299: contig of 795 bp in length
3300 3399: gap of 100 bp
3400 4153: contig of 754 bp in length
4154 4253: gap of 100 bp
4254 4978: contig of 725 bp in length
4979 5078: gap of 100 bp
5079 5815: contig of 737 bp in length
5816 5915: gap of 100 bp
5916 6648: contig of 733 bp in length
6649 7520: contig of 772 bp in length
7521 7620: gap of 100 bp
7621 8347: contig of 727 bp in length
8348 8447: gap of 100 bp
8448 9227: contig of 780 bp in length
9228 9327: gap of 100 bp
9328 10053: contig of 725 bp in length
10054 10153: gap of 100 bp
10154 10868: contig of 717 bp in length
10869 10968: gap of 100 bp
10969 11718: contig of 749 bp in length
11719 11818: gap of 100 bp
11819 12557: contig of 739 bp in length
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16712 16811: gap of 100 bp
16813 17539: contig of 728 bp in length
17540 17639: gap of 100 bp
17640 18351: contig of 712 bp in length
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18452 19163: contig of 711 bp in length
19164 19263: gap of 100 bp
19264 20054: contig of 792 bp in length
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20155 20891: contig of 737 bp in length
20892 20992: gap of 100 bp
20993 21720: contig of 729 bp in length
21721 21820: gap of 100 bp
21821 22553: contig of 733 bp in length
22554 22653: gap of 100 bp
22654 23420: contig of 767 bp in length
23421 23520: gap of 100 bp
23521 24234: contig of 714 bp in length
24235 24334: gap of 100 bp
24335 25069: contig of 735 bp in length

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*	25070	25169:	gap of 100 bp	in length
*	25170	25915:	contig of 746 bp	in length
*	25916	26015:	gap of 100 bp	in length
*	26016	26751:	contig of 736 bp	in length
*	26752	26851:	gap of 100 bp	in length
*	26852	27574:	contig of 723 bp	in length
*	27575	27674:	gap of 100 bp	in length
*	27675	28437:	contig of 763 bp	in length
*	28438	28537:	gap of 100 bp	in length
*	28538	29258:	contig of 721 bp	in length
*	29259	29359:	gap of 100 bp	in length
*	29360	30069:	contig of 710 bp	in length
*	30069	30169:	gap of 100 bp	in length
*	30169	30918:	contig of 750 bp	in length
*	30919	31018:	gap of 100 bp	in length
*	31019	31770:	contig of 752 bp	in length
*	31771	31870:	gap of 100 bp	in length
*	31871	32658:	contig of 788 bp	in length
*	32659	32758:	gap of 100 bp	in length
*	32759	33501:	contig of 743 bp	in length
*	33502	33601:	gap of 100 bp	in length
*	33602	34347:	contig of 746 bp	in length
*	34348	34447:	gap of 100 bp	in length
*	34448	35165:	contig of 718 bp	in length
*	35166	35265:	gap of 100 bp	in length
*	35266	35998:	contig of 733 bp	in length
*	35999	36098:	gap of 100 bp	in length
*	36099	36802:	contig of 704 bp	in length
*	36803	36903:	gap of 100 bp	in length
*	36903	37632:	contig of 730 bp	in length
*	37633	37732:	gap of 100 bp	in length
*	37733	38454:	contig of 722 bp	in length
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*	40214	40948:	contig of 735 bp	in length
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*	41793	41892:	gap of 100 bp	in length
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*	42631	42731:	gap of 100 bp	in length
*	42731	43459:	contig of 729 bp	in length
*	43460	43559:	gap of 100 bp	in length
*	43560	44277:	contig of 718 bp	in length
*	44278	44377:	gap of 100 bp	in length
*	44378	45120:	contig of 743 bp	in length
*	45121	45220:	gap of 100 bp	in length
*	45221	45942:	contig of 722 bp	in length
*	45943	46042:	gap of 100 bp	in length
*	46043	46775:	contig of 733 bp	in length
*	46776	46875:	gap of 100 bp	in length
*	46876	47609:	contig of 734 bp	in length
*	47610	47709:	gap of 100 bp	in length
*	47710	48446:	contig of 737 bp	in length
*	48447	48546:	gap of 100 bp	in length
*	48547	49285:	contig of 739 bp	in length
*	49286	49385:	gap of 100 bp	in length
*	49386	50188:	contig of 793 bp	in length
*	50179	50278:	gap of 100 bp	in length
*	50279	51008:	contig of 730 bp	in length
*	51009	51108:	gap of 100 bp	in length
*	51109	51846:	contig of 738 bp	in length
*	51847	52672:	gap of 100 bp	in length
*	52673	52772:	contig of 726 bp	in length
*	52773	53727:	gap of 100 bp	in length
*	53728	53806:	contig of 733 bp	in length
*	53806	54330:	gap of 100 bp	in length
*	53807	54331:	contig of 725 bp	in length
*	54331	54430:	gap of 100 bp	in length
*	54431	55166:	contig of 736 bp	in length
*	55167	55266:	gap of 100 bp	in length

	Query Match	17.5%	Score 44.2	DB 2	Length 71032	
	Best Local Similarity	44.1%	Pred. No. 24			
	Matches	97	Conservative	0	Mismatches	123; Indels 0; Gaps 0;
OY	*	55267	55979:	contig of 713 bp	in length	
	*	55980	56079:	gap of 100 bp		
	*	56080	56823:	contig of 744 bp	in length	
	*	56824	56923:	gap of 100 bp		
	*	56924	57626:	contig of 703 bp	in length	
	*	57627	57766:	gap of 100 bp		
Dd	3	GCCGGGAGAGCGGCCGGAGTGAAGCCTGATTCGTCTTGCGCGCTCCACCTCCACGCG	62			
Dd	28390	GCCCCNAGGGGGGGGGCGCGNCGNGAGNCCCCTGCGGGCGGAGNCCNCNGGGGCCNNNNNN	2833			
OY	63	CAGAAGCGCCCAACAGAGACCACCATCGATGCCGATTTCCACAGCTTGGGATCAGAGCA	122			
Dd	28330	NGCCGGGCGCGCGCGNAGNCCCCGANNCCNNCCGGGGGGGGGGCGCCGCGCGGNCCCC	2827			
OY	123	GGGACCAAGGAGCCAGAACTGCGCGCGCCCGCCCTCGCTTGGCGCGAGAGAACTCC	182			
Dd	28270	GGGACCGCGGGGGCGCCNNCCCCCGCCCGCGCGCGCCGAGNCGGGGGGGGAGNCCNAGCC	2821			
OY	183	CTCACNAGAGGAAGTCTCCCTCAACCCGAGCCAGCCCTGC	222			
Dd	28210	NGCNCGCCCGCGCGGTCCGATTGTCGTCNTGCNTGCCGCGG	28171			
RESULT 16						
LOCUS	AC022707	88064 bp	DNA	linear	HTG-13-Jul-2000	
DEFINITION	Homo sapiens clone RP11-59L21, LOW-PASS SEQUENCE SAMPLING.					
VERSION	AC022707.2	GI:9146450				
KEYWORDS	HTG: HTGS PHASPO					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1 (bases 1 to 88064) Britten, B., Linton, L., Nusbaum, C. and Lande, E. Homo sapiens chromosome, clone RP11-59L21 Unpublished					
AUTHORS	2 (bases 1 to 88064) Britten, B., Linton, L., Nusbaum, C., Lande, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barua, N., Beckert, R., Bedalov, F., Boguslavsky, I., Boukhalter, B., Brown, A., Burkett, G., Castle, A., Choepel, V., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeRubeis, P., Dewar, K., Domino, M., Doyle, M., Feneberg, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardana, S., Grant, G., Hagos, B., Heath, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lebockzy, J., Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Margulis, N., McManis, P., McGuck, A., McKernan, K., McNetters, R., Meldrum, J., Meneses, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vasilev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.Y., Zimmer, A. and Zody, M.					
TITLE	Direct Submission					
JOURNAL	Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA					
COMMENT	On Jul 13, 2000 this sequence version replaced gi:6522799. All repeats were identified using RepeatMasker: Smt, A.E.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html -----Genome Center Center: Whitehead Institute/ MIT Center for Genome Research Genetic code: WTBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu					

```
----- Project Information
Center project name: L5349
Center clone name: 59_L_21

* NOTE: This record contains 89 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1      857: contig of 857 bp in length
858    157: gap of 100 bp
958    1863: contig of 906 bp in length
1864    1963: gap of 100 bp in length
1964    2869: contig of 906 bp in length
2870    3854: contig of 885 bp in length
3855    3954: gap of 100 bp
3955    4838: contig of 884 bp in length
4839    5830: contig of 892 bp in length
4939    5930: gap of 100 bp
5831    6826: contig of 896 bp in length
5931    6926: gap of 100 bp
6827    7854: contig of 928 bp in length
6927    7954: gap of 100 bp
7855    8854: contig of 900 bp in length
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10931    11813: contig of 883 bp in length
10931    11913: gap of 100 bp
11814    12788: contig of 875 bp in length
12789    13770: contig of 882 bp in length
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13771    13870: gap of 100 bp
13871    14745: contig of 875 bp in length
14746    14845: gap of 100 bp
14846    15751: contig of 906 bp in length
15752    15851: gap of 100 bp
15852    16748: contig of 897 bp in length
16749    16848: gap of 100 bp
16849    17762: contig of 914 bp in length
17763    17862: gap of 100 bp
17863    18750: contig of 888 bp in length
18751    18850: gap of 100 bp
18851    19733: contig of 883 bp in length
19734    19833: gap of 100 bp
19834    20803: contig of 870 bp in length
20804    20903: gap of 100 bp
20904    21815: contig of 912 bp in length
21816    21915: gap of 100 bp
21916    22738: contig of 923 bp in length
22739    22838: gap of 100 bp
22839    23737: contig of 899 bp in length
23738    23837: gap of 100 bp
23838    24702: contig of 865 bp in length
24703    24802: gap of 100 bp
24803    25686: contig of 884 bp in length
25687    25786: gap of 100 bp
25787    26682: contig of 896 bp in length
26683    26782: gap of 100 bp
26783    27686: contig of 904 bp in length
27687    28687: gap of 100 bp
28688    28687: contig of 901 bp in length
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29688    29787: contig of 900 bp in length
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30714    30813: gap of 100 bp
30814    31700: contig of 887 bp in length
31701    31800: gap of 100 bp
31801    32654: contig of 885 bp in length
32655    32754: gap of 100 bp
32755    33671: contig of 911 bp in length
33672    33772: gap of 100 bp
33772    34666: contig of 895 bp in length
34667    34766: gap of 100 bp
34767    35651: contig of 888 bp in length
35652    35751: gap of 100 bp
35752    36620: contig of 869 bp in length
36621    36720: gap of 100 bp
36721    37596: contig of 876 bp in length
37597    37696: gap of 100 bp
37697    38661: contig of 865 bp in length
38662    38661: gap of 100 bp
38662    39533: contig of 872 bp in length
39534    39633: gap of 100 bp
39634    40549: contig of 916 bp in length
40550    40650: gap of 100 bp
40650    41357: contig of 708 bp in length
41358    41457: gap of 100 bp
41458    42385: contig of 928 bp in length
42386    42485: gap of 100 bp
42486    43425: contig of 939 bp in length
43425    43525: gap of 100 bp
43525    44404: contig of 880 bp in length
44405    44504: gap of 100 bp
44505    44505: contig of 901 bp in length
44506    45505: gap of 100 bp
45506    46375: contig of 870 bp in length
46376    46475: gap of 100 bp
46476    47355: contig of 880 bp in length
47356    47455: gap of 100 bp
47456    48340: contig of 885 bp in length
48341    48440: gap of 100 bp
48441    49320: contig of 880 bp in length
49321    49420: gap of 100 bp
49421    50324: contig of 904 bp in length
50325    50424: gap of 100 bp
50425    51321: contig of 897 bp in length
51322    51421: gap of 100 bp
51422    52350: contig of 925 bp in length
52351    52450: gap of 100 bp
52451    53355: contig of 905 bp in length
53356    53455: gap of 100 bp
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61199    61298: gap of 100 bp
61299    62170: contig of 872 bp in length
62171    62271: gap of 100 bp
62271    63184: contig of 914 bp in length
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63285    64181: contig of 897 bp in length
64182    64281: gap of 100 bp
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* 66255 67165: contig of 910 bp in length
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* 68164 68264: gap of 100 bp
* 68264 69159: contig of 895 bp in length
* 69159 69259: gap of 100 bp
* 69259 70132: contig of 873 bp in length
* 70132 70232: gap of 100 bp
* 70232 70332: gap of 100 bp

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Best Local Similarity 47.0%; Pred. No. 24;
Matches 116; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

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QY 61 CGCAGAGAGCGCGCGCGGAGTGAAGCGCTGATCGTCCCTGCGCCCTCCACCTCCCGAGG 120
    |||||
Db 25337 GCGGCGGAGAGCGCGCGGAGTGAAGCGCTGATCGTCCCTGCGCCCTCCACCTCCCGAGG 25396
    |||||

QY 121 CAGGAGACGAGGAGCGCGGAGTGAAGCGCTGATCGTCCCTGCGCCCTCCACCTCCCGAGG 180
    |||||
Db 25397 GCGGCGGAGAGCGCGCGGAGTGAAGCGCTGATCGTCCCTGCGCCCTCCACCTCCCGAGG 25456
    |||||

QY 181 CCCTCACGAGGAGGAGGAGCTCCCTGATCGTCCCTGCGCCCTCCACCTCCCGAGG 240
    |||||
Db 25457 GCGGCGGAGAGCGCGCGGAGTGAAGCGCTGATCGTCCCTGCGCCCTCCACCTCCCGAGG 25516
    |||||

QY 241 AGACCGC 247
    |||||
Db 25517 CGCGGAGC 25523
    |||||

RESULT 17
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LOCUS Mus musculus chromosome 16 clone RP23-104L12, WORKING DRAFT
DEFINITION
AC079420
AC079420.1 GI:9958032
AC079420.1 HTG PHASE1: HTG DRAFT.
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 239130)
DOE Joint Genome Institute.
Sequencing of Mouse
Unpublished
2 (bases 1 to 239130)
DOE Joint Genome Institute.
Direct Submission
Submitted (01-SEP-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 0
Center clone name: RPCI-23_104L12
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Summary Statistics
Consensus quality: 154414 bases at least Q40
Consensus quality: 183510 bases at least Q30
Consensus quality: 194836 bases at least Q20
Estimated insert size: 22300; agarose-fp estimation
Estimated insert size: 233130; sum-of-contigs estimation

```

```

Quality coverage: 3.27 in Q20 bases; agarose-fp estimation
Quality coverage: 3.12 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
consists of 61 contigs. The true order of the pieces is
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 1030: contig of 1030 bp in length
1031 1130: gap of unknown length
1131 2520: contig of 1390 bp in length
2521 2620: gap of unknown length
2621 3633: contig of 1013 bp in length
3634 3733: gap of unknown length
3734 5381: contig of 1648 bp in length
5382 5482: gap of unknown length
5482 6792: contig of 1311 bp in length
6793 6892: gap of unknown length
6893 8478: contig of 1586 bp in length
8479 8578: gap of unknown length
8579 9635: contig of 1056 bp in length
9635 9734: gap of unknown length
9734 10791: contig of 1057 bp in length
10792 10891: gap of unknown length
10891 12358: contig of 1367 bp in length
12359 13771: gap of unknown length
13772 13871: contig of 1413 bp in length
13872 14998: contig of 1127 bp in length
14999 15098: gap of unknown length
15099 16261: contig of 1163 bp in length
16261 17426: gap of unknown length
17427 17526: contig of 1065 bp in length
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18542 20200: contig of 1015 bp in length
20201 20300: gap of unknown length
20301 21424: contig of 1123 bp in length
21425 22553: gap of unknown length
22554 22654: contig of 1030 bp in length
22654 23664: gap of unknown length
23664 24815: contig of 1010 bp in length
24816 24915: gap of unknown length
24916 26356: contig of 1055 bp in length
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27957 28056: contig of 1441 bp in length
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29856 31409: contig of 1809 bp in length
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31510 34198: contig of 1444 bp in length
34199 34298: gap of unknown length
34299 36147: contig of 2689 bp in length
36148 36247: gap of unknown length
36248 37988: contig of 1849 bp in length
37989 38088: gap of unknown length
38089 39156: contig of 1741 bp in length
39157 39256: gap of unknown length
39257 43172: contig of 1066 bp in length
43173 43272: gap of unknown length
43273 44383: contig of 3916 bp in length
44384 44483: gap of unknown length
44484 46827: contig of 1110 bp in length
46828 46927: gap of unknown length
46928 49015: contig of 2344 bp in length
49016 49115: gap of unknown length
49116 51007: contig of 2089 bp in length
51007 51007: contig of 1892 bp in length

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51108	51109	contig of 2812 bp in length
53920	54019	gap of unknown length
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56109	56208	gap of unknown length
56609	59412	contig of 3204 bp in length
59413	59512	gap of unknown length
59513	62565	contig of 3053 bp in length
62566	64722	gap of unknown length
64725	64822	contig of 2059 bp in length
64825	70728	contig of 5904 bp in length
70729	70829	gap of unknown length
70829	74333	contig of 3505 bp in length
74334	74433	gap of unknown length
74434	80096	contig of 5662 bp in length
80096	80196	gap of unknown length
80196	84713	contig of 4518 bp in length
84714	84813	gap of unknown length
84814	86901	contig of 4278 bp in length
86902	86919	gap of unknown length
89192	94478	contig of 5287 bp in length
94479	94578	gap of unknown length
94579	98798	contig of 4220 bp in length
98798	98898	gap of unknown length
98898	103681	contig of 4783 bp in length
103682	103781	gap of unknown length
103782	109611	contig of 5836 bp in length
109618	109717	gap of unknown length
115578	115583	contig of 5872 bp in length
115580	115689	gap of unknown length
122207	122207	contig of 6518 bp in length
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122308	129310	contig of 7003 bp in length
129311	129410	gap of unknown length
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135068	133167	gap of unknown length
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144563	151374	contig of 8722 bp in length
151375	151474	gap of unknown length
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159604	159703	gap of unknown length
159704	162675	contig of 9572 bp in length
162676	163376	gap of unknown length
163376	176542	contig of 7167 bp in length
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176643	186218	contig of 8476 bp in length
186219	186218	gap of unknown length
186219	196151	contig of 9933 bp in length
196152	196251	gap of unknown length
196252	204073	contig of 8822 bp in length
204074	204173	gap of unknown length
204174	210101	contig of 12928 bp in length
210102	212101	gap of unknown length
217202	227352	contig of 10151 bp in length
227353	228452	gap of unknown length
227353	239330	contig of 11678 bp in length

FEATURES											
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/mol_type="genomic DNA"											
/db_xref="taxon:10090"											
/chromosome="16"											
/clone="RP23-104112"											
/clone_11b="RPcl mouse BAC library 23"											
BASE COUNT		63482	a	51866	c	54864	g	59989	t	8929	others
ORIGIN											
Query Match		17.5%	Score		44	DB		2	Length		239130
Best Local Similarity		43.5%	Pred. No.		18				Indels		0
Matches 101; Conservative		0	Mismatch		131				Gaps		0

[illegible]

RESULT 18	AC100379	DNA	1 linear	HTG 28-NOV-2002
AC100379				
DESCRIPTION	Mus musculus clone RP2-11C19, LOW-PASS	SEQUENCE		
VERSION	AC100379..3	GI:25815482		
KEYWORDS	HTG; HTGS PHASED.			
SOURCE	Mus musculus (house mouse)			
ORANISM	Mus musculus			

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS
1 (bases 1 to 59008)	Birren, B., Nusbaum, C. and Lander, E.	Mus musculus, clone RP23-131C19	Unpublished	2 (bases 1 to 59008)	Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., ... et al.

Anderson, S., Barina, N., Basciotti, V., Bogdanavicius, L., Bourkharov, A., Brown, A., Camarata, J., Campopiano, A., Chang, Y., Chazaro, B., Choepel, Y., Colangelo, K., Collins, S., Collymore, A., Cook, A., Cooke, P., Derrillano, K., Dewar, K., Diaz, J.S., Dodde, S., Fairo, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Gilde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hultine, M., Iliev, I., Jones, C., Jones, C., Kama, A., Karatas, A., Kells, C., Lacroque, K., Lamaszars, R., Landers, T., Lehotzky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McNetters, R., Melidoni, J.C., Menus, L., Mhoya, T., Mlenka, J., Murphy, T., Nykro, U., Nygren, C., Nobdu, C., Norman, C.H., O'Connor, L., O'Donnell, P., O'Neill, V., Oliver, J., Peterson, C., Phunkhara, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Ribick, W., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuppick, R., Seaman, S., Severy, J., Spencer, B., Stange-Thomann, S., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Teisseyre, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triglilio, J., Vasiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.-S., Young, G., Zehnon, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Whitehead Institute/MIT Center for Genome  
Submitted (22-NOV-2011)  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
(baes, 1 to 59008)  
Britten, B., Nisbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,

Barrin, N., Birstein, V., Bloom, I., Boguski, Y., L., Sunkin, G.,  
Camata, J., Chang, J., Chazaro, B., Chopely, Y., Collamore, A.,  
Cook, A., Cooke, P., DeArllano, K., Dewar, K., Diaz, J. S., Dodge, S.,  
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,  
Gardya, S., Gord, S., Graham, L., Grand-Pierre, N., Hatze, N.,  
Hagob, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,  
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,  
Landrat-Toth, K., Liu, G., McLean, C., McDonald, P., Major, J.,  
Matthews, C., McCarthy M., Meldrum, J., Meneses, L., Mihova, T.,  
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,  
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,  
Peterson, K., Phunhuan, P., Pierre, A., Raymond, C., Retta, R.,  
Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schnepack, R.,



TITLE  
JOURNAL  
COMMENT

Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N.,  
Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Toppan, K.,  
Treviers, M., Vasseliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,  
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M.  
Direct Submission  
Submitted (28-NOV-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Nov 28, 2002 this sequence version replaced g1:24962776.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute / MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@genome.wi.mit.edu

----- Project Information

Center project name: 131\_C\_19

Center clone name: 131\_C\_19

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\* NOTE: This record contains 74 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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3215 3214: gap of 100 bp  
3925 3924: contig of 711 bp in length  
4026 4025: gap of 100 bp  
4728 4727: contig of 703 bp in length  
4829 4828: gap of 100 bp  
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5639 5638: gap of 100 bp  
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11916 11915: gap of 100 bp  
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12817 12816: contig of 705 bp in length  
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13623 13622: contig of 682 bp in length  
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16786 17467: contig of 682 bp in length  
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37472 37471: gap of 100 bp  
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38274 38273: gap of 100 bp  
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39772 39771: contig of 705 bp in length  
39873 39872: gap of 100 bp  
40562 40561: contig of 690 bp in length  
40663 40662: gap of 100 bp  
41372 41371: contig of 710 bp in length  
41473 41472: gap of 100 bp  
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44713 44712: gap of 100 bp  
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Db 57809 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 57868
QY 97 GTTGCACAGGTCTGTGATCAGAGGACAGAGACAGAGAGCCAGAGAACTGCGCGCCCGCGC 156
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QY 157 CCGTGGCCCTGGCGGAGAGAACTCTCTCACGAGAGAACTCTCTCACCGCGCCGAC 216
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RESULT 21
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AC022663
AC022663.2 GI:9139598
VERSION      AC022663.2
KEYWORDS      HTG; HTGS; PHASEO.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 63082)
AUTHORS      Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE      Homo sapiens, clone RP11-2905
JOURNAL      Unpublished
AUTHORS      2 (bases 1 to 63082)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Bonislawski,L., Bonhagalter,B., Brown,A., Burkett,G., Castle,A.,
Chospel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Dearellano,K., Dewar,K., Domino,M., Doyle,M., Fensholt,U.,
Ferreira,P., Fitzhugh W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Harford,A., Horton,L.,
Howard,J.C., Johnson,R., Jones,C., Kann,L., Karas,A., Klein,J.,
Lander,E., Lebeckzy,J., Levine,R., Lien,C., Liu,G., Locke,K.,
Macdonald,F., Meldrum,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
Pierre,N., Pisanl,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Rohmann,N.,
Stojanovic,N., Sudranaman,A., Talamas,D., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submision
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:910643.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4854
Center clone name: 29_O_5

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*****
NOTE: This record contains 77 individual
sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
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[illegible]

http://www.chori.org/bacpac/home.htm  
VECTOR: PBAC3.6  
IMPORTANT: This sequence is not the entire insert of clone RP11-330C15. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-330C15 is at 157264 in this sequence. The true left end of clone RP11-465C24 is at 130978 in this sequence. The true right end of clone RP11-153J24 is at 100 in this sequence.

## FEATURES

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VERSION AC079109.1 GI:9845151
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 65225)
            Homo sapiens chromosome 11, clone RP11-461A14
            Unpublished
            2 (bases 1 to 65225)
            Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
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            Zimmer, A. and Zody, M.
            Direct Submission
            Submitted (18-AUG-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)

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http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10783
Center clone name: 461_A_14

* NOTE: This record contains 79 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
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* 39542 39641: gap of 100 bp
* 39642 40375: contig of 734 bp in length
* 40376 40475: gap of 100 bp
* 40476 41178: contig of 703 bp in length
* 41179 41278: gap of 100 bp
* 41279 42024: contig of 746 bp in length
* 42025 42124: gap of 100 bp
* 42125 42869: contig of 745 bp in length
* 42870 42969: gap of 100 bp
* 42970 43705: contig of 736 bp in length
* 43706 43805: gap of 100 bp
* 43806 44533: contig of 728 bp in length
* 44534 45348: gap of 715 bp in length
* 45349 45448: gap of 100 bp
* 45449 46178: gap of 100 bp
* 46179 46278: contig of 730 bp in length
* 46279 46378: gap of 100 bp
* 46379 47012: contig of 734 bp in length
* 47013 47112: gap of 100 bp
* 47113 47842: contig of 730 bp in length
* 47843 47942: gap of 100 bp
* 47943 48673: contig of 731 bp in length
* 48674 48773: gap of 100 bp
* 48774 49497: contig of 724 bp in length
* 49498 49597: gap of 100 bp
* 49598 50328: contig of 731 bp in length
* 50329 50428: gap of 100 bp
* 50429 51172: contig of 744 bp in length
* 51173 51272: gap of 100 bp
* 51273 51984: contig of 712 bp in length

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Query Match 17.2% Score 43.4; DB 2; Length 65225;
Best Local Similarity 44.5%; Pred. No. 34;
Matches 110; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

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OY 1 CGGCGGGGAGCGCGCGGAGTGAAGCTGATCTGCTTGGGCGCTCCACCTCCCGAGG 60
DB 56814 CGCGCGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 56755
OY 61 CGCGAGAGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 56754 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 56695
OY 121 CAGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 56694 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 56635
OY 181 CCTCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 56634 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 56575
OY 241 AGACCGG 247
DB 56574 CGGCGCG 56568

```

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RESULT 24
AC143979 129264 bp DNA linear HTG 09-APR-2003
LOCUS AC143979
DEFINITION Macaca mulatta clone CH250-272017, *** SEQUENCING IN PROGRESS ***.
ACCESSION AC143979.1 GI:29649555
VERSION AC143979.1
KEYWORDS HTG; HTGS_PHASE2; HTGS_PGI.
SOURCE Macaca mulatta (rheseus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
1 (bases 1 to 129264)
AUTHORS Cuiros, M. and Mlosoavljic, A.
TITLE Pooled genomic indexing (PGI): mathematical analysis and experiment
design
JOURNAL (in) Guigo, R. and Gusfield, D. (Eds.);
ALGORITHMS IN BIOFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI
2002, ROME, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS: 10-28;
Springer (2002)
2 (bases 1 to 129264)
REFERENCE Mlosoavljic, A., Sodergren, B., Cuiros, M., Li, B., Jackson, A.R.,
Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Albrooks, S.L.,
Amaratunga, H.C., Aye, J.R., Ayala, M., Banks, T., Barbieri, J.,
Benton, J., Bivins, K., Blumhagen, K., Bonin, D., Bouck, J.,
Bowle, S., Brievas, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
Burke, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carion, T.F.,
Chen, Z., Chen, M., Cavaros, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Cox, C., Coyle, M.D., Chowdhury, I., Christopoulos, C., Cleveland, C.D.,
Davy, Carroll, L., DeDertich, D.A., Delaney, K.R., Delgado, O.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthett, K.O., Draper, H.,
Dugan-Rocha, S., Durbin, K.J., Egan, A., Barnhart, C., Edwards, C.C.,

```



```

Elhaj, C., Emerling, S., Escotto, M., Falle, T., Ferraguto, D.,
Fligny, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J.,
Garcia, A., Garner, T., Garza, N., Gill, R., Gottlieb, J. H., Guayra, W.,
Gunnarsson, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K.,
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Howard, S., Huber, J., Huliyil, S., Hume, J., Ioshihashi, I., Jackson, L. E.,
Jacobson, B., Jia, Y., Johnson, R., Jolyet, S., Joudh, S.,
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Lewin, J., Li, J., Li, Z., Lichtenberg, O., Lieu, C., Liu, J., Liu, M.,
Loudisek, H., Lozano, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Ma, J., Maneshwari, M., Mapa, P., Marondei, I., Martin, R.,
Martindale, A., Martinez, E., Massey, E., Mamhney, E., McLeod, M. P.,
Meador, M., Mei, G., Mercher, S., Metzger, M., Miller, A., Miner, G.,
Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K. T., Morgan, M.,
Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N.,
Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S.,
Ogulu, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
Peet, J., Perez, L., Peters, L., Pickens, R., Pirmus, E., Pu, L. L.,
Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojokokan, I., Rolfe, M.,
Ruiz, S., Saverly, G., Scherer, S., Scott, G., Shen, H., Shih, C.,
Shooshari, N., Sisson, I., Sodergren, E., Sonaite, T., Sparks, A.,
Stanley, H., Stone, H., Sutton, A., Svatek, A., Taber, P., Tamerisa, A.,
Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B.,
Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D.,
Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R.,
Washington, C., Wallington, S., Williams, G., Williamson, A.,
Wieszyk, R., Woodson, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J.,
Zorilla, S., Zuchetapatti, R., Weinstein, G. and Gibbs, R.

Direct Submission
3 (bases 1 to 129264)
Worley, K. C.

JOURNAL
REFERENCE
AUTHORS
JOURNAL
TITLE

COMMENT
-----
Center: Baylor College of Medicine
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
-----
Project Information
Center project name: CH250-272017
Center clone name: CH250-272017
-----
Summary Statistics
Chemistry: Dye-Primer Bodyfly: inf of reads
Chemistry: Dye-Terminator Big Dye: inf of reads
Consensus quality: 7907 bases at least Q40
Consensus quality: 9526 bases at least Q30
Consensus quality: 11065 bases at least Q20
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/cembank_draft_data.html)
* NOTE: The contigs are based on the application
* of the PGI method using the Human genome (NCBI build 31)
* as the comparative genome.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* Location/Qualifiers
1 129264: contig of 129264 bp in length.
FEATURES
source
1. 129264
/organism="Macaca mulatta"
/mol_type="genomic DNA"
/db_xref="taxon:9544"

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misc_feature
1. 129264
/notes="assembly name: CH250-272017.1B
CONFIDENCE: 0.83"

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BASE COUNT 4678 a 3424 c 3768 g 4138 t 113256 others
ORIGIN

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Query Match 17.2% Score 43.4; DB 2; Length 129264;
Best Local Similarity 48.7%; Pred. No. 26;
Matches 116; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

```

```

1 CGCGCCGAGGAGCGCGCGCGAGTGAAGCTGATCGTCTCGCGCTCCACTCCCGAGG 60
4013 CGCGCCGAGGAGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4072
DB 61 CGGAGAGGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
4073 CGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4132
DB 121 CAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAG 180
DB 4133 CGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4192
DB 181 CCTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 238
DB 4193 GGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4250

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RESULT 25
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LOCUS Drosophila melanogaster chromosome 3 clone BACR02H01 (D735) RPCT-98
DEFINITION 02.H.1 map 94D-94D strain Y cn bw sp.*** SEQUENCING IN PROGRESS
*** 94 unordered pieces.
AC008193
VERSION AC008193.10 GI:19482329
KEYWORDS HTG, HTG_PHASE1.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 154607)
Celniker, S. E., Agbayani, A., Arcaina, T. T., Baxter, E., Blazej, R. G.,
Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C. M., Farfan, D. E., Galle, R., George, R. A., Harris, N. L.,
Hinkle, A., Hoskins, R. A., Houston, K. A., Hummasti, S. R., Katta, K.,
Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A. R.,
Moshrefi, M., Nixon, K., Pacleab, J. M., Park, S., Pfeiffer, B.,
Richards, S., Sethi, H., Swirskas, R. R., Wan, K. H., Webster, D.,
Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G. M.
Sequencing of Drosophila melanogaster
Unpublished
2 (bases 1 to 154607)
Celniker, S. E., Agbayani, A., Arcaina, T. T., Baxter, E., Blazej, R. G.,
Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C. M., Farfan, D. E., Galle, R., George, R. A., Harris, N. L.,
Hoskins, R. A., Houston, K. A., Hummasti, S. R., Katta, K., Kearney, L.,
Kim, E., Lee, B., Lewis, S., Li, P., Lomocan, M. A., Mazda, P.,
Moshrefi, A. R., Moshrefi, M., Nixon, K., Pacleab, J. M., Park, S.,
Pfeiffer, B., Rich, R., Rubin, G. M., Sequiera, A., Sethi, H., Shih, E.,
Swirskas, R. R., Wan, K. H., Weinburg, T., Zhang, R., Zierman, L. B. and
Rubin, G. M.
Direct Submission
Submitted (29-JUL-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
3 (bases 1 to 154607)
Celniker, S. E., Agbayani, A., Arcaina, T. T., Baxter, E., Blazej, R. G.,
Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C. M., Farfan, D. E., Galle, R., George, R. A., Harris, N. L.,
Hinkle, A., Hoskins, R. A., Houston, K. A., Hummasti, S. R., Katta, K.,
Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A. R.,
Moshrefi, M., Nixon, K., Pacleab, J. M., Park, S., Pfeiffer, B.,
Pfeiffer, B., Rich, R., Rubin, G. M., Sequiera, A., Sethi, H., Shih, E.,
Swirskas, R. R., Wan, K. H., Weinburg, T., Zhang, R., Zierman, L. B. and
Rubin, G. M.

```

TITLE  
JOURNAL  
COMMENT

Richards, S., Sethi, H., Svirskas, R.R., Man, K.H., Webster, D.,  
Woolliey, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.  
Submitted (15-MAR-2002) Drosophila Genome Center, Lawrence Berkeley  
Laboratory, MS 64-121, Berkeley, CA 94720 USA  
On Mar 15, 2002 this sequence version replaced gi:5957934.  
For further information about this sequence, including its location  
and relationship to other sequences, please visit our sequence  
archive web site (<http://www.fruitfly.org/sequence/>) or send email  
to [bdg@fruitfly.berkeley.edu](mailto:bdg@fruitfly.berkeley.edu). All contigs in this submission meet  
the following cutoffs: length >= 200 bases.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 94 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

26774 27574: contig of 801 bp in length  
27575 27575: gap of unknown length  
27576 27576: gap of 910 bp in length  
28565 28564: gap of unknown length  
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30050 30049: contig of unknown length  
30130 30129: gap of unknown length  
31676 31675: contig of 1546 bp in length  
31756 31755: gap of unknown length  
33381 33381: contig of 1626 bp in length  
33382 33381: gap of unknown length  
33462 34951: contig of 1490 bp in length  
34952 34951: gap of unknown length  
35032 35031: gap of unknown length  
36243 36243: contig of 1132 bp in length  
36244 36243: gap of unknown length  
38078 38078: contig of 1835 bp in length  
38079 38078: gap of unknown length  
38158 38158: gap of unknown length  
38159 38158: contig of 1795 bp in length  
39534 40033: gap of unknown length  
40034 40033: gap of 949 bp in length  
40083 41062: gap of unknown length  
41063 41062: gap of 1950 bp in length  
43013 43012: gap of unknown length  
43093 43092: gap of unknown length  
44794 44793: contig of 1701 bp in length  
44874 44873: gap of unknown length  
46732 46731: gap of 1858 bp in length  
46812 46811: gap of unknown length  
48753 48752: contig of 1941 bp in length  
48833 48832: gap of unknown length  
50461 50461: gap of 1629 bp in length  
50542 50541: gap of unknown length  
52859 52858: contig of 2317 bp in length  
52939 52938: gap of unknown length  
54832 54831: contig of 1893 bp in length  
54912 54911: gap of unknown length  
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56619 56618: gap of unknown length  
57857 57856: gap of unknown length  
57937 57936: gap of 1158 bp in length  
60796 60795: gap of unknown length  
60875 60875: gap of 2859 bp in length  
60976 60975: gap of unknown length  
62729 62728: contig of 1853 bp in length  
62809 62808: gap of unknown length  
65905 65904: gap of 3096 bp in length  
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68417 68416: gap of unknown length  
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72335 72334: gap of unknown length  
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77111 77110: gap of unknown length  
77111 77110: gap of 4451 bp in length  
81642 81641: gap of unknown length  
81722 81721: gap of 3627 bp in length  
85349 85348: gap of unknown length  
85428 85428: gap of unknown length  
86976 86976: gap of 1548 bp in length  
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92459 92459: contig of 5403 bp in length  
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92460 92459: gap of 6577 bp in length  
99116 99116: gap of unknown length  
99117 99116: gap of 5523 bp in length  
104719 104719: gap of unknown length  
11051 11051: contig of 6252 bp in length  
111052 111051: gap of unknown length  
11132 11131: gap of 3608 bp in length  
114740 114739: gap of unknown length  
114819 114819: gap of 2645 bp in length  
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117545 117544: gap of 7867 bp in length  
125411 125411: contig of unknown length  
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125432 125431: gap of 7082 bp in length  
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132574 132573: gap of unknown length  
132574 132573: contig of 607 bp in length







JOURNAL Submitted (02-MAY-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
 (E-mail:tsasak@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)  
 On May 15, 2002 this sequence version replaced gi:18146331. Genes were predicted from the integrated results of the following: GENSSCAN 1.0, BLAST2.0, BLASTX2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr  
 (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologues of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative', and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.  
 The orientation of the sequence is from -21M13 to M13rev of the BAC clone. This sequence of B1108H10 clone has an overlap with B1075D06 (DBJ: AP003202) clone at the position 1 to 34,607 of 5' end and an overlap with B1003B09 (AP004222) at the position of 133,578 to 136,357 of 3' end. Detailed information of this entry is assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/GenomeSeq.html>.

## FEATURES

## source

location/Qualifiers

1..136357  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="genomic DNA"  
 /cultivar="Nipponbare"  
 /db\_xref="taxon:39947"  
 /chromosome="1"

## gene

## CDS

join(3241..3533,3588..3865,3966..4238,4548..4589,4745..4758)  
 /gene="B1108H10.1"  
 /clone="B1108H10"  
 /note="hypothetical protein"

## gene

## misc\_feature

7428..8396

## gene

## CDS

probably inactive due to stop codon(s) in CDS

## gene

## CDS

probably inactive due to no termination codon in CDS

similar to Oryza sativa chromosome 1, P0035H10.7"  
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 join(9310..9551,9618..9636)  
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 /codon\_start=1  
 /protein\_id="BAB92720.1"

## gene

## CDS

/db\_xref="GI:20805046"  
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 join(13008..13165,13238..13306,14712..14850,15804..15978,  
 15996..16158,20154..20346)  
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 join(13008..13165,13238..13306,14712..14850,15804..15978,  
 15996..16158,20154..20346)  
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 /note="contains ESTs AU092422 (C50524), C26948 (C50524)  
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## gene

## CDS

/protein\_id="BAB92721.1"  
 /db\_xref="GI:20805047"  
 /translation="MAAETPAAGSGVILKHIIVLAPKEVTPERLDLIRGFGVLNVL  
 VPSKRAEPCGCAPEVRLCGCPVSVASVTRGRTIGFLIMFVTHEIIPALCKRNGK  
 YMRKGMFPMGCHIIILHKQWPGVETORANMAGGQGNNGVARSPEAGETDMADG  
 TTSKRSVANDMSVSGVGVOLHRRROTITAGNGDGRVDEHVIASGRHYPFLSM  
 ELTPAMNPSGSGELCWGTPVSIENMHGFTHPCECTFESTEGVKEYIEHPALIEPAK  
 ELTAMKELTIDMPTFVAVNS"  
 join(21107..21155,22151..22202,22551..22571,22614..22729,  
 23798..24168)  
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 join(21107..21155,22151..22202,22551..22571,22614..22729,  
 23798..24168)  
 /note="hypothetical protein  
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## LTR

## gene

## misc\_feature

/protein\_id="BAB92722.1"  
 /db\_xref="GI:20805048"  
 /translation="MOELDERDRLMSESPRYLTSSROQSLPPRIRARLPPRYTWYV  
 SITLVADIDANERTHTILNRPWSSCRAVNVLVPRSEVAVREITTHPEEDQT  
 CRIISRTPEVAVEIAITHPEEDQASIIISQTPEVAVEIAITHPEENORASRIIR  
 TPMEVAVEIAITHPEENORASRIIRTPMEVVV"  
 complement(21910..22638)  
 /note="3' LTR"  
 complement(25812..31005)  
 /gene="B1108H10.6"  
 complement(25812..31005)  
 /gene="B1108H10.6"  
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 similar to Oryza sativa chromosome 1, P0489A01.2"

## gene

## misc\_feature

/pseudo  
 complement(32316..35620)  
 /gene="B1108H10.7"  
 complement(32316..35620)  
 /gene="B1108H10.7"  
 /note="TNP-like transposable element  
 probably inactive due to frameshift(s) in CDS  
 probably inactive due to no termination codon in CDS  
 pseudogene"

## LTR

## gene

## CDS

complement(36659..37386)  
 /note="5' LTR"  
 join(38213..38361,40249..40441)  
 /gene="B1108H10.8"  
 join(38213..38361,40249..40441)  
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## LTR

## gene

## misc\_feature

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 IDYKPTIVNS"  
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 /note="5' LTR"  
 43777..48553  
 /gene="B1108H10.9"  
 43777..48553

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/gene="B1108H10.9"
/note="Probably inactive due to stop codon(s) in CDS
pseudogene, gag-pol polyprotein"
pseudo
48457..49360
/note="3' LTR"
LTR
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/note="hypothetical protein"
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/db_xref="gi:20805050"
/translation="MACOLTPPPPLASNVGGAIALITSPGALVMPPLPMS
GVGHKMPNSMADSSSVPAFLIICALAAVATSPGASISINTG"
complement(join(52294..52412,53301..53436,54501..54609,
54602..57489,58077..58378,58667..58864))
/gene="B1108H10.11"
complement(join(52294..52412,53301..53436,54501..54609,
54602..57489,58077..58378,58667..58864))
CDS
Query Match 17.0%; Score 42.8; DB 8; Length 136357;
Best Local Similarity 48.5%; Pred. No. 35;
Matches 116; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 7 GGGAGCGCGCCGGAGTGAGCGCTGATGTCCTGCGCGCTTCACTTCCCGAGCGAGA 66
DB 13954 GGGAGCGCGCGAGGAGCTGTGTGCGGAGCCACCGCGCCGCAATCCCGCGCGAGCG 14013
QY 67 AGCGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 126
DB 14014 CCTCGCCATCGCGCGCGCTTCCCTGCTCTCCGCGCGAGAGAGAGAGAGAGAG 14073
QY 127 CCAGGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 186
DB 14074 GATGGAGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 14133
QY 187 CCNAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 245
DB 14114 CCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 14192

RESULT 30
AP005633 155328 bp DNA linear HTG 08-AUG-2002
LOCUS Oryza sativa (japonica cultivar-group) chromosome 9 clone P0463G11,
DEFINITION *** SEQUENCING IN PROGRESS ***
ACCESSION AP005633.1 GI:22138857
VERSION AP005633.1
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 Sasaki, T., Matsumoto, T. and Katayose, Y.
Oryza sativa nipponbare (GAG) genomic DNA, chromosome 9, PAC
clone: P0463G11
Published Only in Database (2002)
2 (bases 1 to 155328)
Submitted (07-AUG-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rsgp.dna.affrc.go.jp/,
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
NOTE: It currently consists of 1 contig. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is

```

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available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
FEATURES
source
1..155328
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="9"
/clones="P0463G11"
BASE COUNT 42283 a 33769 c 34451 g 44142 t 683 others
ORIGIN
Query Match 17.0%; Score 42.8; DB 2; Length 155328;
Best Local Similarity 52.4%; Pred. No. 34;
Matches 97; Conservative 0; Mismatches 87; Indels 1; Gaps 1;

QY 1 CGGCGCGGAGAGCGCGCGAGTAGCGCTGATGTCCTGCGCGCTTCACTTCCCGAG 60
DB 87963 CGGCGCGGAGAGCGCGCGAGTAGCGCTGATGTCCTGCGCGCTTCACTTCCCGAG 88022
QY 61 CGGAG-AGGCGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 119
DB 88023 CAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 88082
QY 120 GCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 179
DB 88083 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 88142
QY 180 TCCCT 184
DB 88143 CGCCT 88147

RESULT 31
AC020769 175493 bp DNA linear HTG 26-MAR-2000
LOCUS Homo sapiens clone RP11-11M3, WORKING DRAFT SEQUENCE, 20 unordered
DEFINITION
ACCESSION AC020769
VERSION AC020769.4 GI:7329384
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 175493)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome, clone RP11-11M3
Unpublished
2 (bases 1 to 175493)
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Allen, N.,
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collamore, A., Cooke, P.,
DeArrelano, K., Dewar, K., Domino, M., Doyle, M., Fensholt, J.,
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J., Johnson, R., Jones, C., Kam, L., Karas, R., Klein, J.,
Lander, J., Lechocsky, J., Levine, R., Liu, C., Liu, G., Locke, K.,
Macdonald, P., Margulis, N., McEwan, P., McGuire, A., McKernan, K.,
Mehner, R., Menzies, J., Menzies, L., Morrison, J., Nelson, K.,
Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K.,
Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Strange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talama, J., Teste, S., Theodore, J.,
Tirrell, A., Vasiliyev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W., J.,
Zimmerman, A. and Zody, M.
Direct Submission
Submitted (09-JAN-2000) Whitehead Institute/MIT Center for Genome

```





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RESULT 32
AC010550 LOCUS AC010550 197926 bp DNA linear HTG 04-SEP-2000
DEFINITION Homo sapiens chromosome 16 clone RPI1-550L9, WORKING DRAFT
ACCESSION AC010550
VERSION AC010550.7 GI:9966237
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE DOB Joint Genome Initiative.
JOURNAL Sequencing of Human Chromosome 16
AUTHORS Unpublished
TITLE 2 (bases 1 to 197926)
DOE Joint Genome Institute.
DIRECT SUBMISSION Direct Submission
SUBMITTED (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Sep 4, 2000 this sequence version replaced gi:9954629.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: G17836
Center clone name: RPCI-11_550L9
-----
Summary Statistics
Consensus quality: 167417 bases at least Q40
Consensus quality: 181828 bases at least Q30
Consensus quality: 187575 bases at least Q20
Estimated insert size: 184660; agarose-fp estimation
Estimated insert size: 196626; sum-of-contigs estimation
Quality coverage: 5.84 in Q20 bases; agarose-fp estimation
Quality coverage: 5.84 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
consists of 12 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
* * *
1 1438: contig of 1438 bp in length
1439 1538: gap of unknown length
1539 2567: contig of 1029 bp in length
2568 2667: gap of unknown length
2668 3793: contig of 1126 bp in length
3794 3894: gap of unknown length
3894 6548: contig of 2655 bp in length
6549 6648: gap of unknown length
6648 11592: contig of 4944 bp in length
11593 11692: gap of unknown length
11693 17217: contig of 5525 bp in length
17218 17318: gap of unknown length
17318 24917: contig of 7600 bp in length
24918 25017: gap of unknown length
25017 36743: contig of 11726 bp in length
36744 36844: gap of unknown length
36844 60051: contig of 23208 bp in length
60052 60152: gap of unknown length
60152 96861: contig of 36710 bp in length
96862 130048: gap of unknown length
130048 130147: contig of 33086 bp in length
130148 197926: contig of 67779 bp in length.
Location/Qualifiers
1..197926

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[illegible]

Quality: Phrap Quality >=40 100% of Sequence,  
Estimated Total Number of Errors is 0.  
NOTE: BACTERIAL TRANSPOSON excised at 62920.

FEATURES	Location/Qualifiers
source	1. .198253

BASE COUNT	52657	a	47264	c	46791	g	51541	t
ORIGIN	.	.						

Accession	Sequence	Position
QY	63 CAGAAAGCGCCCAACGAGAACCCCACTGCGCCGACGCTTGAGTCAAGGCA	122
QY	171081 CAGAAAGCTCCCGCTCGCTCCCACTTCCTCCCACTCCCGCTCTCGGCGGAGAG	171022
QY	123 GGGACACGAGGACCGAGAACTGGCGCGCGCGCGCGCGCTGCGCGAGAGAAAGTCC	182
Db	171021 GAGGCCCAAGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGAGAAACCGAAC	170962
QY	183 CTCAACGAGAGAAAGCTCCCTCAACCCGCGCGCAAGCCTTGCAAGGGGGGCGCTGAGGTCA	242
Db	170961 CCGAGCGGCTTGAGAGCGCAACGAGCGGCGCGCGCGCGCGCGCGCGCTGAGCCTG	170902
QY	243 ACC 245	
Db	170901 TTC 170899	

RESULT 34  
AC023825/c  
-20000000  
317531 bp DNA linear PRI 01-DEC-2002

LOCUS	AC003882	21,324 bp	2001	.....	complete sequence:
DEFINITION	Homo sapiens chromosome 16 clone RP11-322D4, complete sequence:				
ACCESSION	AC003882				
VERSION	AC003882.8	GI:2589046			
KEYWORDS	HTG.				
SOURCE	Homo sapiens (human)				

Estimated Total Number of Errors is 0.7.  
Location/Qualifiers

```

FEATURES
source      location/Qualifiers
1. .217521 /cran1sm="Homo sapiens"

```

BASE COUNT	55314	a	54228	c	54570	g	53409	e
ORIGIN								

Qy	63	TACAAAGCCGCCCAACGAGAACCCCCCAATGCCCCGACGTTGGCAAGGTCTGAGATCAGAGGCA	122
Db	86769	CAGGAAGCTCCGCGCTCGCTCCCACTTCCTCTCCCACTCCCTCTCTCGGCGGAGGGAG	86710
Qy	123	GGGACCGAGGAGACCGAGAACTGGGGCGGGCGGGCGGCTCGCTCGGCGGAGGAAAGCTCC	182
Db	86709	GAGGCCCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAGAGAGAACCGGAC	86505
Qy	183	CTCAACGAGAGGAAGCTTCCTCTCAACCGCGGCGCAAGCTGTAGGGGGGGCGCGTGGGCTCAG	242
Db	86649	CCGAGCGGCTGGGAGGCCACGCGAGCGGGCCGTGGCGCGCGCGGAGCGCGCTGAAGCTCG	86590
Qy	243	ACC 245	
Db	86589	TCC 86587	

LOCUS	AC108553	250348 bp	DNA	linear	fig 13-1941-2005
DEFINITION	Rattus norvegicus clone CH230-225D10, WORKING DRAFT SEQUENCE.				

REFERENCE  
AUTHORS

1 (baes 1 to 250348)  
Muzny D.,Mairle, Metzker,M.Lee, Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Albrooks,S., Amn,A., Arguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Bader,H., Baldwin,D., Bandaranaike,D., Barber,M., Bannstead,M., Benahmed,F., Bivaldo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Bunay,C., Burck,P., Butrell,K., Calderon,E., Carstens,V., Carter,K., Cavazos,T., Cesaar,H., Centen,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D Souza,, Davila,M.L., Davis,C., Davy-Carrillo,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dihn,H., Diya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durkin,C., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,P., Fraser,C.M., Gabisi,A., Gante,R., Garcia,A., Garner,T., Garza,M., Geiergeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamli,C., Hamilton,C., Hamilton,K., Harvey,Y., Haylak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,J., Hollins,B., Howells,S., Huylk,S., Hume,J., Idlibird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jollivet,A., Karpeth,S., Kelly,S., Kelly,S., Khan,Z., Kling,L., Kovar,Z., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,Y., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lourenswela,L., Loulsegad,H., Lozado,R.J., Lu,X., Ma,J., Meeshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Manguna,A., Mangum,B., Mapua,P., Martin,K., Martin,E., Martinez,E., McWhinney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,

[illegible]

```

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GKQX
Center clone name: CH230-225D10
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 233602 bases at least Q40
Consensus quality: 236433 bases at least Q30
Consensus quality: 238558 bases at least Q20
Estimated insert size: 248554; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_direct.html).
* NOTE: This is a working draft sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced

```

	* by the finished sequence as soon as it is available and
	* * the accession number will be preserved.
FEATURES	1 250348: contig of 250348 bp in length. Location/Qualifiers 1. 250348
source	/organism="Rattus norvegicus" /mol_type="genomic DNA" /db_xref="taxon:10116" /clone="CH230-225D10" 8097..10377
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misc_feature	178075..179620 /note="wgs_contig"
BASE COUNT	63843 a 55099 c 54333 g 67221 t 9852 others
ORIGIN	
Query Match	17.0%; Score 42.8; DB 2; Length 250348; Best Local Similarity 48.9%; Pred. No. 29;
Matches 113; Conservative	0; Mismatches 118; Indels 0; Gaps 0;
Oy	12 GGCGCCGGGAGTGAAGGCGCTGTATCTCTCCTTGCGGCCTCACCTCCCCAGGCGCAAAAGGCG 71
Db	201073 GGCGGGGGCGGGCTCTTCCTTCCCAGAGAGGGGGGCCAACTCAAACGGGCGCTTCGGGCA 201132
Oy	72 CCACAGAGAACCCCGAGTCCCGAGCGTTGCCACGCTCTGGAGATCAGAAGGAGGACAG 131
Db	201133 CTTCGCCCGAGCTCTCGGCTCGATTCTGATCTCGGGGGGGGGCGGGCGGCCGCCCGGGGGCGGGT 201192
Oy	132 GAGCCAGGAAGTCTGCGCGCGCGCGCGCGCGCGCGCTTGCGCGAGGAGAACTCTCCATCCANNA 191
Db	201193 GGCGCGAGAGCTGGGGGGGCGCTTCCCAATGAGCGCGCGCGCGCGCTTGTCTGCGCCGG 201252
Oy	192 GGGAACTCTCCCTCAACCAGCGCCCAAGCCTCTGAGAGGGGGCGCGTGGGCTCA 242
Db	201253 GCCGCCCTTCCCCCAGCGCGCGCGCGCGCTTCCCCCGAGAGCTCTCGG 201303
RESULT 36	
LOCUS	AC099852 67126 bp DNA linear HTG 22-NOV-2001
AC099852	Mus musculus clone RP23-13502, LOW-PASS SEQUENCE SAMPLING.
DEFINITION	AC099852 GI:17047217
ACCESSION	AC099852.1
VERSION	HTG; HTGS_PHASE0.
KEYWORDS	Mus musculus (house mouse)
SOURCE	Mus musculus
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 Birren,B., Linton,L., Nusbaum,C. and Lander,E. Unpublished
AUTHORS	2 (bases 1 to 67126) Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boughalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,K., D'Amico,S., Collamore,A., Cook,A., Cook,P., DeLallano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferrara,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Grinde S., Gord S., Goylette,M., Graham,I., Grand-pierre,N., Hagoe,R., Hearford,A., Horton,T., Hultine W., Iliev,I., Johnson,R., Jones,C., Kamet,A., Karatas,A., Kells,C., LaRoque,K., Lamarates,R., Landers,T., Lehotzky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Major,J., Margulis,N., Matthews,C., McCarthy,M., McKean,P., McKeenan,K., McNeeters,R., Meldrum,U., Meneus,L., Milnova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nordhu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Olivier,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Rella,R., Riback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N.,
TITLE	
JOURNAL	
REFERENCE	
AUTHORS	

TITLE  
JOURNAL  
COMMENT

Straus, N., Subramanian, A., Talamas, J., Tefaye, S., Theodore, J.,  
Toppan, K., Travels, M., Travis, N., Trigglio, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, C.,  
Zainoun, U., Zembek, L., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L13335  
Center clone name: L33\_O\_2

-----  
\* NOTE: This record contains 83 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1  
702 1801: contig of 701 bp in length  
802 1801: gap of 100 bp  
1516 1515: contig of 714 bp in length  
1616 1515: gap of 100 bp  
2336 2336: contig of 721 bp in length  
2437 2436: gap of 100 bp  
3109 3109: contig of 673 bp in length  
3210 3209: gap of 100 bp  
3941 3940: contig of 731 bp in length  
4041 4040: gap of 100 bp  
4706 4705: contig of 665 bp in length  
4806 4805: gap of 100 bp  
5493 5493: contig of 688 bp in length  
5594 5593: gap of 100 bp  
6283 6282: contig of 689 bp in length  
7059 7059: contig of 677 bp in length  
7159 7159: gap of 100 bp  
7860 7860: contig of 701 bp in length  
7960 7960: gap of 100 bp  
8675 8675: contig of 715 bp in length  
8775 8775: gap of 100 bp  
9504 9504: contig of 729 bp in length  
9604 9604: gap of 100 bp  
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10392 10392: gap of 100 bp  
11039 11039: contig of 712 bp in length  
11104 11103: gap of 100 bp  
11919 11919: contig of 715 bp in length  
12019 12019: gap of 100 bp  
12741 12741: contig of 722 bp in length  
12841 12841: gap of 100 bp  
13539 13539: contig of 698 bp in length  
13640 13639: gap of 100 bp  
14341 14341: contig of 702 bp in length  
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16893 16893: gap of 100 bp  
17617 17617: contig of 724 bp in length

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17718 18416: contig of 639 bp in length  
18417 18516: gap of 100 bp  
18517 19200: contig of 684 bp in length  
19201 19300: gap of 100 bp  
19301 20030: contig of 730 bp in length  
20031 20130: gap of 100 bp  
20131 20895: contig of 765 bp in length  
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22541 22640: gap of 100 bp  
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23380 23480: gap of 100 bp  
23481 24321: contig of 741 bp in length  
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24322 24321: contig of 680 bp in length  
24322 25002: gap of 100 bp  
25002 25102: contig of 710 bp in length  
25102 25911: gap of 100 bp  
25911 26629: contig of 718 bp in length  
26629 26729: gap of 100 bp  
26730 27454: contig of 725 bp in length  
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27555 28265: contig of 711 bp in length  
28266 28365: gap of 100 bp  
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29067 29165: gap of 100 bp  
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29867 29966: gap of 100 bp  
29967 30705: contig of 739 bp in length  
30706 30805: gap of 100 bp  
30806 31511: contig of 706 bp in length  
31512 32337: contig of 726 bp in length  
32338 33170: gap of 100 bp  
33171 33270: contig of 733 bp in length  
33271 33680: gap of 100 bp  
33680 34090: contig of 720 bp in length  
34091 34810: gap of 100 bp  
34811 34910: gap of 100 bp  
34910 35634: contig of 724 bp in length  
35634 35735: gap of 100 bp  
35735 36437: contig of 703 bp in length  
36437 36538: gap of 100 bp  
36538 37245: contig of 708 bp in length  
37245 37345: gap of 100 bp  
37346 38039: contig of 694 bp in length  
38040 38139: gap of 100 bp  
38140 38895: contig of 756 bp in length  
38896 38995: gap of 100 bp  
38996 39723: contig of 728 bp in length  
39724 39823: gap of 100 bp  
39824 40533: contig of 710 bp in length  
40534 40633: gap of 100 bp  
40634 41364: contig of 731 bp in length  
41365 41464: gap of 100 bp  
41465 42170: contig of 706 bp in length  
42171 42270: gap of 100 bp  
42271 42995: contig of 725 bp in length  
42996 43085: gap of 100 bp  
43086 43787: contig of 692 bp in length  
43787 43887: gap of 100 bp  
43888 44576: contig of 689 bp in length  
44577 44677: gap of 100 bp  
44678 45386: contig of 710 bp in length  
45387 45486: gap of 100 bp  
45487 46195: contig of 709 bp in length  
46196 46295: gap of 100 bp  
46296 46987: contig of 692 bp in length  
46988 47087: gap of 100 bp



16182	16943:	contig of 762	bp	in	length
16944	17643:	contig of 100	bp	in	length
17044	17768:	contig of 725	bp	in	length
17769	18668:	gap of 100	bp	in	length
17869	18613:	contig of 745	bp	in	length
18514	18713:	gap of 100	bp	in	length
18714	18460:	contig of 747	bp	in	length
19461	15560:	gap of 100	bp	in	length
19561	20328:	contig of 768	bp	in	length
20329	20428:	gap of 100	bp	in	length
20439	21151:	contig of 723	bp	in	length
21152	22017:	gap of 100	bp	in	length
22018	22117:	gap of 100	bp	in	length
22118	22817:	contig of 755	bp	in	length
22817	22972:	gap of 100	bp	in	length
22973	23743:	contig of 771	bp	in	length
23744	23843:	gap of 100	bp	in	length
23844	24684:	contig of 741	bp	in	length
24685	24684:	gap of 100	bp	in	length
24685	25443:	contig of 759	bp	in	length
25444	25543:	gap of 100	bp	in	length
25544	26370:	contig of 727	bp	in	length
26371	26370:	gap of 100	bp	in	length
26371	27124:	contig of 754	bp	in	length
27125	27324:	gap of 100	bp	in	length
27325	27980:	contig of 756	bp	in	length
27981	28080:	gap of 100	bp	in	length
28081	28811:	contig of 731	bp	in	length
28812	28911:	gap of 100	bp	in	length
28912	29655:	contig of 784	bp	in	length
29656	29795:	gap of 100	bp	in	length
29796	30568:	contig of 773	bp	in	length
30569	30568:	gap of 100	bp	in	length
30669	31488:	contig of 770	bp	in	length
31489	31538:	gap of 100	bp	in	length
31539	32278:	contig of 740	bp	in	length
32279	32378:	gap of 100	bp	in	length
33378	33208:	contig of 730	bp	in	length
33109	33208:	gap of 100	bp	in	length
33209	33956:	contig of 748	bp	in	length
33957	34056:	gap of 100	bp	in	length
34057	34840:	contig of 784	bp	in	length
34841	34940:	gap of 100	bp	in	length
34941	35674:	contig of 734	bp	in	length
35675	35774:	gap of 100	bp	in	length
35775	36534:	contig of 760	bp	in	length
36535	36634:	gap of 100	bp	in	length
36635	37400:	contig of 766	bp	in	length
37401	37500:	gap of 100	bp	in	length
37501	38289:	contig of 789	bp	in	length
38290	38389:	gap of 100	bp	in	length
38390	39247:	contig of 758	bp	in	length
39148	39247:	gap of 100	bp	in	length
39248	40007:	contig of 760	bp	in	length
40008	40107:	gap of 100	bp	in	length
40108	40835:	contig of 728	bp	in	length
40836	40935:	gap of 100	bp	in	length
40936	41677:	contig of 742	bp	in	length
41678	41777:	gap of 100	bp	in	length
41778	42547:	contig of 770	bp	in	length
42548	42647:	gap of 100	bp	in	length
42648	43385:	contig of 738	bp	in	length
43386	43485:	gap of 100	bp	in	length
43486	44281:	contig of 766	bp	in	length
44282	44351:	gap of 100	bp	in	length
44352	45108:	contig of 757	bp	in	length
45109	45208:	gap of 100	bp	in	length
45209	45573:	contig of 765	bp	in	length
45974	46673:	gap of 100	bp	in	length
46074	46642:	contig of 769	bp	in	length
46843	46542:	gap of 100	bp	in	length
46943	47592:	contig of 750	bp	in	length

[illegible][illegible]

RESULT 38	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
EX088698	230413 bp DNA linear HTG 04-JUN-2003
Mus musculus chromosome X clone RP23-309D15, *** SEQUENCING IN	
PROGRESS ***, 7 unordered pieces.	
EX088698	
EX088698.5 GI:11442026	
HTG; HTG PHASE1; HTGS DRAFT; HTGS_FULLTOP.	
Mus musculus (house mouse)	
Mus musculus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
1 (bases 1 to 230413)	
McLaren,S.	
Direct Submission	
Submitted (03-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,	
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:	
hmmquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk	
On Jun 5, 2003 this sequence version replaced gi:29125140.	
Consent to publish: I agree that this work has been made available in the	
public domain by submitting to the NCBI genome project and I agree that	
the copyright for this work is retained by me, but the copyright license for	
this work is transferred to NCBI. I understand that any request to remove	
the copyright from this work will be granted by NCBI. I understand that any	
request to change the copyright for this work will be granted by NCBI.	

Sequence from the Mouse genome sequencing consortium. Sequence data  
shotgun may have been used to confirm this sequence.  
from the whole genome shotgun alone has only been used where it has  
a phred quality of at least 30.



Fri Nov 7 08:10:00 2003

us-10-081-817a-19\_copy\_1\_252.rge

Page 44

```
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2150)
          Uchimura,K., Muramatsu,H., Kadomatsu,K., Kannagi,R., Habuchi,O. and
          Muramatsu,T.
TITLE Polypeptide of N-acetylglucosamine-6-O-sulfotransferase and DNA
       encoding the same
JOURNAL Patent: US 6455289-A 1 24-SEP-2002;
FEATURES Location/Qualifiers
          source 1..2150
            /organism="unknown"
BASE COUNT 386 a 695 c 679 g 390 t
ORIGIN
Query Match 16.7%; Score 42.2; DB 6; Length 2150;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 104; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 28 CCTGATGCTCCCTGCGCCCTCCACCTCCCGAGGCGGAGAGGCGCCACAGAGACCCCA 87
Db 143 CCGGTCCTCTCTCGAGCCCGCTGCTCATGGAGAGCAGCCCTGGGCGCGGGGACAGCA 202
QY 88 GTGCCCGACGTTGCCACGATCTGGGATCAAGAGGAGGAGCCAGAGAACTGGCGC 147
Db 203 GCCTCTGCGCGCGCGCGCGCGCTCGATGCGGCGCCCGCCAGTCCGCGCCGCGAGCGGCC 262
QY 148 CGCCCCCGCCCTGCGCCCTGCGCGCGAGGAGAACTCTCTACCGAGAGGAACTCCCTCAC 207
Db 263 TGCAGCGTCCCGCTCTCTGCGGCTGCGAGGCGCGCTCTCGCGCGCGCGCGCGCGCTGTG 322
QY 208 CCGGCCCGACCTGCGAGGAGGAGGCGCGCTG 235
Db 323 CTTGTGATGAGCCGCGAGCTGCGCGCGAG 350
```

Search completed: November 6, 2003, 08:07:07  
Job time : 1536.45.secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 06:12:36 ; Search time 182.882 Seconds  
(without alignments)  
3719.648 Million cell updates/sec

Title: US-10-081-817a-19\_COPY\_1\_252

Perfect score: 252

Sequence: 1 cggccgggagagcgccggg.....gtggggtcagaccgaagc 252

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: N\_Geneseq\_19Jun03:\*  
2: /SIDSI/gcgdata/geneseq/emb1/NA1980.DAT:\*  
3: /SIDSI/gcgdata/geneseq/emb1/NA1981.DAT:\*  
4: /SIDSI/gcgdata/geneseq/emb1/NA1982.DAT:\*  
5: /SIDSI/gcgdata/geneseq/emb1/NA1983.DAT:\*  
6: /SIDSI/gcgdata/geneseq/emb1/NA1984.DAT:\*  
7: /SIDSI/gcgdata/geneseq/emb1/NA1985.DAT:\*  
8: /SIDSI/gcgdata/geneseq/emb1/NA1986.DAT:\*  
9: /SIDSI/gcgdata/geneseq/emb1/NA1987.DAT:\*  
10: /SIDSI/gcgdata/geneseq/emb1/NA1988.DAT:\*  
11: /SIDSI/gcgdata/geneseq/emb1/NA1989.DAT:\*  
12: /SIDSI/gcgdata/geneseq/emb1/NA1990.DAT:\*  
13: /SIDSI/gcgdata/geneseq/emb1/NA1991.DAT:\*  
14: /SIDSI/gcgdata/geneseq/emb1/NA1992.DAT:\*  
15: /SIDSI/gcgdata/geneseq/emb1/NA1993.DAT:\*  
16: /SIDSI/gcgdata/geneseq/emb1/NA1994.DAT:\*  
17: /SIDSI/gcgdata/geneseq/emb1/NA1995.DAT:\*  
18: /SIDSI/gcgdata/geneseq/emb1/NA1996.DAT:\*  
19: /SIDSI/gcgdata/geneseq/emb1/NA1997.DAT:\*  
20: /SIDSI/gcgdata/geneseq/emb1/NA1998.DAT:\*  
21: /SIDSI/gcgdata/geneseq/emb1/NA1999.DAT:\*  
22: /SIDSI/gcgdata/geneseq/emb1/NA2000.DAT:\*  
23: /SIDSI/gcgdata/geneseq/emb1/NA2001A.DAT:\*  
24: /SIDSI/gcgdata/geneseq/emb1/NA2001B.DAT:\*  
25: /SIDSI/gcgdata/geneseq/emb1/NA2002.DAT:\*  
26: /SIDSI/gcgdata/geneseq/emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	143.6	57.0	1794	24	ABT06542
2	42.2	16.7	1951	22	AAH43895
3	42.2	16.7	2150	20	AAH87820
4	41.4	16.4	3431	22	AAH98302
5	41.4	16.4	3459	24	AAH29756
6	40.8	16.2	2666	24	ABZ53386
7	39.6	15.7	868	21	AAH65433
8	38.6	15.3	840	24	ABL60745

c	9	38.4	15.2	222	22	AAH65077	Novel human polynu
c	10	38.4	15.2	3106	25	ACC46319	Human dltip zinc f
c	11	38.4	15.2	3690	25	ACC46404	Human dltip zinc f
c	12	38.4	15.2	42999	24	ABH65032	Invertebrate forag
c	13	38.2	15.2	528	22	AAH30761	Megalomycin polyke
c	14	38.2	15.2	114955	20	AAH53491	Human adenosine A1
c	15	38.2	15.1	1875	20	AAH35383	CDNA encoding HTHB
c	16	38	15.1	2875	25	ABH90552	Human kinase CDNA
c	17	38	15.1	4890	20	AAH34648	Promoter containin
c	18	37.8	15.0	1947	24	ABH99879	Human CDNA encloidi
c	19	37.8	15.0	1947	25	ABH99879	Human kinase CDNA
c	20	37.8	15.0	1965	24	ABH99878	Human CDNA encloidi
c	21	37.8	15.0	1965	25	ABH99878	Human kinase CDNA
c	22	37.8	15.0	2341	24	AAH30551	Human kinase polyD
c	23	37.8	15.0	2595	24	ABH90875	Human CDNA encloidi
c	24	37.8	15.0	2595	25	ABH90875	Human kinase CDNA
c	25	37.8	15.0	2613	24	ABH90874	Human CDNA encloidi
c	26	37.8	15.0	2613	25	ABH90874	Human kinase CDNA
c	27	37.8	15.0	2670	25	ABH90545	Human CDNA encloidi
c	28	37.8	15.0	2670	24	ABH90544	Human kinase CDNA
c	29	37.8	15.0	2688	25	ABH99882	Human CDNA encloidi
c	30	37.8	15.0	2688	24	ABH90544	Human kinase CDNA
c	31	37.8	15.0	2856	25	ABH99891	Human CDNA encloidi
c	32	37.8	15.0	2856	24	ABH90553	Human kinase CDNA
c	33	37.8	15.0	2874	24	ABH99890	Human CDNA encloidi
c	34	37.8	15.0	2931	25	ABH99887	Human CDNA encloidi
c	35	37.8	15.0	2931	24	ABH90549	Human kinase CDNA
c	36	37.8	15.0	2949	25	ABH99886	Human CDNA encloidi
c	37	37.8	15.0	2949	24	ABH90548	Human kinase CDNA
c	38	37.8	15.0	5418	19	AAH94191	Promoter region of
c	39	37.8	15.0	35100	20	AAH73802	KSHV LTR DNA (nucl
c	40	37.8	15.0	137507	17	AAH91941	KSHV long unique c
c	41	37.6	14.9	1731	19	AAH10106	Maize UDP-glucose
c	42	37.6	14.9	4257	19	AAH68520	The nucleotide seq
c	43	37.6	14.9	4257	19	AAH68520	Infected cell prot
c	44	37.4	14.8	2461	22	AAH44725	Novel protein kina
c	45	37.4	14.8	3400	22	AAH51952	Human polynucleoti

#### ALIGNMENTS

RESULT 1	ABT06542	standard; DNA; 1794 BP.
ID	ABT06542	
XX	ABT06542;	
AC	07-NOV-2002 (first entry)	
XX		
DT	Human HIN-1 coding sequence.	
XX		
DE	Human HIN-1 coding sequence.	
XX		
KW	Human; methylated gene; methylation; breast cancer; marker; WT-1;	
KW	cell proliferative disorder; TWIST; HOXA5; NES-1; RARbeta; cyclin D2;	
KW	retinoic acid receptor beta; oestrogen receptor; Wilms' tumour;	
KW	14.3.3 sigma; HIN-1; RASBP1A; tumour suppressor gene; hypermethylation;	
KW	gene; promoter; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	MO200259347-A2.	
XX		
PD	01-AUG-2002.	
XX		
PF	28-JAN-2002; 2002MO-US02455.	
XX		
PR	26-JAN-2001; 2001US-0771357.	
XX		
PA	(UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.	
XX		
PI	Sukumar S, Eylon E, Doolley WC, Sacchi N, Davidson N, Fackler MJ;	
XX	WPI: 2002-599803/64.	



RESULT 3  
 AAX87820 standard; cDNA; 2150 BP.  
 ID AAX87820  
 AC AAX87820;  
 XX  
 XX 09-NOV-1999 (first entry)  
 DT  
 DE Mouse N-acetylglucosamine-6-O-sulfotransferase cDNA.  
 XX  
 XX N-acetylglucosamine-6-O-sulfotransferase; mouse; GLYCAM-1;  
 KW L-selectin ligand; ss.  
 KM  
 OS Mus musculus.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 470..1921  
 FT /\*tag= a  
 XX  
 XX EP943688-A2.  
 XX  
 XX 22-SEP-1999.  
 XX  
 XX 04-MAR-1999; 99EP-0301530.  
 XX  
 XX 24-JUN-1998; 98JP-0177844.  
 PR 05-MAR-1998; 98JP-0054007.  
 XX  
 XX (SEK) SEIKAGAKU CORP.  
 XX  
 XX Habuchi O, Kadomatsu K, Kannagi R, Muramatsu H,  
 PI Muramatsu T, Uchimura K;  
 XX  
 XX WPI: 1999-520337/44.  
 DR P-PSDB; AAY31656.  
 XX  
 XX New polypeptide of N-acetylglucosamine-6-O-sulfotransferase, useful  
 PT for synthesis of sugar chains, e.g. GLYCAM-1  
 XX  
 XX Claim 5; Page 21-23; 41pp; English.  
 PS  
 XX This is the nucleotide sequence of an isolated cDNA coding for  
 CC mouse N-acetylglucosamine-6-O-sulfotransferase (see AAY31656), an  
 CC enzyme capable of transferring a sulfate group from a sulfate group  
 CC donor to a hydroxyl group at the 6 position of an N-acetylglucosamine  
 CC residue located at the non-reducing end of an oligosaccharide  
 CC represented by the formula GlcNAc-beta1-3Gal-beta1-4GlcNAc, where  
 CC GlcNAc = N-acetylglucosamine residue, Gal = galactose residue,  
 CC beta 1-3 = beta 1-3 glycosidic linkage, and beta 1-4 = beta 1-4  
 CC glycosidic linkage. The cDNA was isolated from a mouse embryo  
 CC cDNA library by PCR amplification. The enzyme is useful for the  
 CC synthesis of sugar chains such as GLYCAM-1, a ligand of L-selectin  
 CC that is involved in homing of lymphocytes and rolling of leukocytes  
 CC occurring at the early stage of inflammation. DNA encoding the  
 CC enzyme is expected to be used for the large-scale production of  
 CC N-acetylglucosamine-6-O-sulfotransferase, or artificial synthesis  
 CC of GLYCAM-1 using transformants which harbour the DNA.  
 XX  
 SQ Sequence 2150 BP; 386 A; 695 C; 679 G; 390 T; 0 other;  
 Query Match 16.7%; Score 42.2; DB 20; Length 2150;  
 Best Local Similarity 50.0%; Pred No. 1.7; Indels 0; Gaps 0;  
 Matches 104; Conservative 0; Mismatches 104;  
 QY 28 CCGATATGTCCTCCGCGCCCTCCACCTCCCGAGCGAGAGGCCCGACAGAGACCCCA 87  
 DB 143 CCAAGTCTCTTCGAGACCGCTGCTCATGAGAGACCGCCCTGCGCGGAGACAGCA 202  
 QY 88 GTGCGCCAGCTTGGCAAGCTGTGGGATCAAGAGGAGGAGCCAGAGACCACTGCGC 147  
 DB 203 GCTCTGTCCGCGCGCGCGCTCGAGTGGCGGCGCCCACTCCGAGCGCGCGCGCC 262

QY 148 CGCCCCCGCCCTGCGCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207  
 DB 263 TCGAGCGTCCCT 322  
 QY 208 CCGGCGCCAGCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 235  
 DB 323 CCGTGTGATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 350

RESULT 4  
 AAH98302/C  
 ID AAH98302 standard; cDNA; 3431 BP.  
 XX  
 XX AAH98302;  
 XX  
 XX 12-OCT-2001 (first entry)  
 DT  
 DE Human EST-derived coding sequence SEQ ID NO: 159.  
 XX  
 XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder;  
 KW biodiversity; gene therapy; nutrition; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200154477-A2.  
 XX  
 XX 02-AUG-2001.  
 XX  
 XX 25-JAN-2001; 2001WO-US02687.  
 XX  
 XX 25-JAN-2000; 2000US-0491404.  
 PR 17-JUL-2000; 2000US-0617746.  
 PR 03-AUG-2000; 2000US-0631451.  
 PR 15-SEP-2000; 2000US-0663870.  
 XX  
 XX (HISE-) HISEQ INC.  
 XX  
 XX Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V,  
 PI Cao Y, Dmanac RA, Zhang J, Wehrman T;  
 XX  
 XX WPI: 2001-476164/51.  
 DR P-PSDB; AAM23643.  
 XX  
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use -  
 XX  
 XX Claim 1; Page 282-283; 1275pp; English.  
 PS  
 XX The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC for forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
 CC of the invention.  
 XX  
 SQ Sequence 3431 BP; 524 A; 1312 C; 1105 G; 490 T; 0 other;  
 Query Match 16.4%; Score 41.4; DB 22; Length 3431;  
 Best Local Similarity 53.4%; Pred No. 2.6; Indels 0; Gaps 0;  
 Matches 87; Conservative 0; Mismatches 76;  
 QY 1 CGGCGGAGAGGCGCGCGGAGTGAAGCTGATCTCTCCGCGCCCTCCACCTCTCCAG 60  
 DB 170 CGGCGGAGAGGCGCGCGGAGTGAAGCTGATCTCTCCGCGCCCTCCACCTCTCCAG 111  
 QY 61 CGGAGAGGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
 DB 110 CGGAGAGGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 51

**QY** 121 CAGGGACCAAGGAGCCAGGAATGCCCGCCCCCGCCCTGCC 163  
||| ||| ||| ||| ||| |||  
**Dd** 50 GAGGCGGC GCCGCGCAGTGC GGAGCGGAGCGCCGCGCGCC 8  
|

RESULT 5
AAD29756/c
ID AAD29756 standard; DNA; 3459 BP

DT 17-MAY-2002 (first entry)

DE Human hyperpolarisation-activated cyclic nucleotide-gated channel 2 DNA.

KM Human; hyperpolarisation-activated cyclic nucleotide-gated channel; HCN;  
 KM therapy; stroke; ichthemia; head injury; epilepsy; Alzheimer's disease;  
 KM Parkinson's disease; learning disorder; memory; attention disorder; pain  
 KM gut disorder; irritable bowel syndrome; IBS; sleep disorder; nootropic;  
 KM neuroprotective; cerebroprotective; antiinflammatory; anticonvulsant;  
 KM tranquilliser; vasotropic; da.

OS Homo sapiens.

FH	Key	Location/Qualifiers
FT	CDS	54..2723

PN WO200202630-A2

PD 10-JAN-2002.

03-JUL-2001; 2001WO-GB02959.

PR 03-JUL-2000; 2000GB-0016360.

PR 03-NOV-2000; 2000GB-0026946.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Strijbos PJLM, Bates S, Gloger I, Davies C;

WPI; 2002-188422/24.

PT New HCN channel polypeptides and polynucleotides which encode the  
PT polypeptides, for the manufacture of compositions to treat stroke  
PT ischemia, head injury, epilepsy, Alzheimer's disease, Parkinson's

Claim 7; Page 52-53; 68pp; English.

The invention relates to new uses of human hypohalastation-activated, cyclic nucleotide-gated ion channel polypeptides and their polymorphic alleles. The HCN channel type I and polynucleotides can be employed as diagnostic reagents to treat stroke/ischemia, head injury, epilepsia, Alzheimer's disease, Parkinson's disease, learning or memory, and attention disorders. These compounds may also be used in treating pain, gut disorders, in particular irritable bowel syndrome (IBS) or sleep disorders. HCN polynucleotides and polypeptides may also be employed as diagnostic reagents for detection of mutations in the above stated diseases. The present sequence is human HCN2 channel DNA.

Sequence 3459 BP: 569 A: 1317 C: 1094 G: 479 T: 0 other: XX

Query Match	16.4%	Score 41.4	DB 24	Length 3459
Best Local Similarity	53.4%	Pred. No. 2.6		
Matches 87	Conservative	0	Memorables	76
			Indels	0
			Gaps	0

1 CGAGCGGGGAGGCGAGCGGGAGTGAGGCTGATCGTCCCTGGGCGCTCACCTCCCGAGG 60  
 170 CGAGCGGGGAGGCGAGCGGGAGTGAGGCTGATCGTCCCTGGGCGCTCACCTCCCGAGG 111  
 170 CGAGCGGGGAGGCGAGCGGGAGTGAGGCTGATCGTCCCTGGGCGCTCACCTCCCGAGG 111

QY      61 CGCAGAAAGCGGCCACGAGAACCCCACTGGCCGCAAGTTGCACGGTCTGGGATCAAGG    120  
         |     |     |     |     |     |     |     |     |     |     |     |     |     |  
Db      110 CGCGGGGTTCGGCCCGGGCTTCTCCCGGGCGCCCGCCGCCCCCGGGCGGTCATTGGC    51

QY 121 CAGGACCCAGGAGCCAGAACTGCGCCGCCGCCCTGCC 163  
Db 50 GAGCGGGCGCGGGCAGTGCAGCGGAGCCGCCGCCGCCGCC 8

RESULT 6  
ABZ35386  
ID ABZ35386 standard; cDNA; 2666 BP

DT 05-FEB-2003 (first entry)

DE	Human gene expression profile polynucleotide SEQ ID NO 497.
DE	

KM Human, artery; endothelium; umbilical; vein; aorta, pulmonary artery;  
KM bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;  
KM tumour; microarray; genome mapping; antiviral; antifungal;  
KM gene expression; gene, ss.

OS Homo sapiens.

PN WO200274979-A2.

PD 26-SEP-2002.

PF 20-MAR-2002; 2002WO-US08456.  
XX

PR 20-MAR-2001; 2001US-276947P.

PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.

PI Wan J, Wang Y,

DR WPI; 2002-740862/80.

PT New Gene expression profile generated from primary, endothelial  
PT epithelial, and muscle cell types, useful for identifying disease  
PT pathologies involving alterations of gene expression, e.g. cancer  
XS Disclosure; Page 638-639; 850p; English.

CC The invention relates to a gene expression

The invention relates to a gene expression profile comprising one or more genes (ABZ31869-ABZ31692), and generated from a cell type. The cell type is a coronary artery endothelium, umbilical artery or vein endothelium, aortic endothelium, dermal microvascular endothelium, pulmonary artery endothelium, myometrium microvascular endothelium, keratinocyte epithelium, bronchial epithelium, mammary epithelium, prostate epithelium, renal cortical epithelium, renal proximal tubule epithelium, small airway epithelium, renal epithelium, umbilical artery smooth muscle, muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle, dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes, aortic smooth muscle, mesangial cells, coronary artery smooth muscle, bronchial smooth muscle, uterine smooth muscle, lung fibroblast, osteoblasts or prostate stromal cell. The gene expression profile is used for determining the level of RNA expression for a sample, determining the phenotype of a cell and distinguishing cell types. The gene or a protein expression profile is useful in identifying disease pathologies involving alterations of gene expression. The assessment of expression profiles may provide meaningful information with respect to tumour type and stage, treatment method and prognosis. The gene or protein expression profile may also be used for creating microarrays. The microarray is useful for genetic and physical mapping of genomes, DNA sequencing, genetic or medical diagnosis, genotyping of organisms, confirming cell or tissue identifications and in identifying promising antibiotics, antiviral or antifungal agents.

Sequence 2666 BP: 591 A: 810 C: 822 G: 443 T: 0 other:  
XX





PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
XX WPI; 2003-129518/12.  
DR P-PSDB; ABR41379.  
XX  
XX Novel human diagnostic and therapeutic polypeptide useful for  
PT identifying test compound which specifically binds to a polypeptide  
PT encoded by human diagnostic and therapeutic polynucleotide, and to  
PT induce antibodies -  
XX  
XX Claim 2; SEQ ID No 240; 591bp; English.  
XX  
XX The invention relates to novel human diagnostic and therapeutic  
CC polynucleotides designated dithp (ACC46080-ACC46749) and to their  
CC encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates  
CC to polynucleotide sequences at least 90% identical to the dithp cDNA  
CC sequences of the invention; recombinant vectors, host cells and  
CC transgenic organisms comprising a dithp nucleic acid sequence; the  
CC recombinant production of DITHP proteins; antibodies specific for DITHP  
CC proteins; microarrays comprising dithp nucleic acid sequences; methods  
CC of detecting dithp nucleotide and protein sequences; methods of screening  
CC for compounds which specifically bind a DITHP protein; and methods of  
CC assessing the toxicity of test compounds using a dithp hybridisation  
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the  
CC diagnosis of a wide variety of conditions including cancer and other cell  
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
CC disorders; neurological disorders; gastrointestinal disorders; transport  
CC disorders; and connective tissue disorders. They may also be used to  
CC screen for modulators of protein activity or gene expression. DITHP  
CC proteins can additionally be used in analysis of the proteome of a tissue  
CC or cell type and to induce antibodies. The dithp nucleic acids are  
CC additionally useful in somatic or germline gene therapy of the disorders  
CC mentioned above, as a source of antisense sequences, as a source of  
CC probes and primers, in genotyping and identification of individuals, in  
CC the generation of transgenic animal models of human disease or knock in  
CC humanised animals, in toxicological testing, and in transcript imaging.  
CC The present sequence represents a dithp cDNA encoding a DITHP protein  
CC which has zinc finger-type transcriptional regulatory activity.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 3106 BP; 896 A; 726 C; 770 G; 714 T; 0 other;  
SQ  
XX  
XX Query Match 15.2%; Score 38.4; DB 25; Length 3106;  
XX Best Local Similarity 57.5%; Pred. No. 11;  
XX Matches 69; Conservative 0; Mismatches 51; Indels 0; Gaps 0;  
QY 42 GCGCCTCACTCCCGAGGCGGAGAGGCGCCAGAGAGCCCGAGTCCCGAGCTTGC 101  
DB 257 GCGAGGCCACACAGCGGCGCCGCGAGGGTGGCCCGGAGGAAACGCTGGCCCGCGTTCA 198  
QY 102 CAGCGTCTGGATTCAGAGGAGGAGCAGAGGAGCAGGAACTGCGCCGCCCGCCCTGTG 161  
DB 197 CAGGCGGCGGCGGCGAGAGCCAGAGGAGGAGGCGTGGCGGACCGGAGAGGCGCTTG 138

KW neurological disorder; gastrointestinal disorder; transport disorder;  
KW connective tissue disorder; drug screening; proteome analysis;  
KW gene therapy; antineoplastic therapy; genotyping; transgenic animal; knock in;  
KW disease model; toxicological testing; transcript imaging;  
KW zinc finger; transcriptional regulator; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200297031-A2.  
XX  
XX 05-DEC-2002.  
XX  
XX 27-MAR-2002; 2002WO-US10056.  
XX  
XX 28-MAR-2001; 2001US-279619P.  
XX 29-MAR-2001; 2001US-280067P.  
XX 29-MAR-2001; 2001US-280068P.  
XX 16-MAY-2001; 2001US-281280P.  
XX 17-MAY-2001; 2001US-291829P.  
XX 17-MAY-2001; 2001US-291849P.  
XX 19-JUN-2001; 2001US-299428P.  
XX 20-JUN-2001; 2001US-299776P.  
XX 20-JUN-2001; 2001US-300001P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
XX Dufour GE, Hillman JT, Yu JY, Tuason O, Yap PE, Amshay SR;  
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
XX WPI; 2003-129518/12.  
XX P-PSDB; ABR41466.  
XX  
XX Novel human diagnostic and therapeutic polypeptide useful for  
PT identifying test compound which specifically binds to a polypeptide  
PT encoded by human diagnostic and therapeutic polynucleotide, and to  
PT induce antibodies -  
XX  
XX Claim 2; SEQ ID No 325; 591bp; English.  
XX  
XX The invention relates to novel human diagnostic and therapeutic  
CC polynucleotides designated dithp (ACC46080-ACC46749) and to their  
CC encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates  
CC to polynucleotide sequences at least 90% identical to the dithp cDNA  
CC sequences of the invention; recombinant vectors, host cells and  
CC transgenic organisms comprising a dithp nucleic acid sequence; the  
CC recombinant production of DITHP proteins; antibodies specific for DITHP  
CC proteins; microarrays comprising dithp nucleic acid sequences; methods  
CC of detecting dithp nucleotide and protein sequences; methods of screening  
CC for compounds which specifically bind a DITHP protein; and methods of  
CC assessing the toxicity of test compounds using a dithp hybridisation  
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the  
CC diagnosis of a wide variety of conditions including cancer and other cell  
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
CC disorders; neurological disorders; gastrointestinal disorders; transport  
CC disorders; and connective tissue disorders. They may also be used to  
CC screen for modulators of protein activity or gene expression. DITHP  
CC proteins can additionally be used in analysis of the proteome of a tissue  
CC or cell type and to induce antibodies. The dithp nucleic acids are  
CC additionally useful in somatic or germline gene therapy of the disorders  
CC mentioned above, as a source of antisense sequences, as a source of  
CC probes and primers, in genotyping and identification of individuals, in  
CC the generation of transgenic animal models of human disease or knock in  
CC humanised animals, in toxicological testing, and in transcript imaging.  
CC The present sequence represents a dithp cDNA encoding a DITHP protein  
CC which has zinc finger-type transcriptional regulatory activity.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX

SQ Sequence 3690 BP; 1086 A; 821 C; 848 G; 935 T; 0 other;

Query Match 15.2%; Score 38.4; DB 25; Length 3690;  
Best Local Similarity 57.5%; Pred. No. 11;  
Matches 69; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 42 GCGCCCTCCACCTCCCGAGGCGGAGGCGCCACAGAGACCCCACTGCGCGACGTTGC 101  
DB 257 GCGAGGCTCCACACGCGCGCGGAGGCTGGCCCGGAGGAAAGCTGGCCCGCGCTTCA 198  
QY 102 CACGCTCTGGGATCTAGAGGCGGAGGCGCCAGGAGCCCACTGCGCGCGCGCGCTG 161  
DB 197 CAGGCGGCGGCGCGGAGGCGGAGGCGGCGCTCGCGACCGCGACCGAGCGCGCGCTG 138

RESULT 12  
AB65032/C  
ID AB65032 standard; DNA; 42999 BP.

AC AB65032;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Invertebrate foraging behaviour associated human DNA sequence #12.  
XX  
KW Attention deficit hyperactivity disorder; ADHD; hypertension;  
KW Invertebrate foraging behaviour; nitric oxide; hypotensive;  
KW GMP-dependent protein kinase; human; neuroleptic; ds;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200259370-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 13-DEC-2001; 2001WO-US48087.  
XX  
PR 15-DEC-2000; 2000US-0738630.  
XX  
PA (NEUR-) NEUROSCIENCES RES FOUND INC.  
XX  
PI Greenspan RJ, Shaw PJ;  
XX  
DR WPI; 2002-636544/68.

PT Identifying a compound that modulates an attention deficit  
PT hyperactivity disorder (ADHD) for treating e.g. ADHD or hypertension,  
PT comprises measuring a foraging behaviour an invertebrate -  
XX  
XX  
PS Claim 89; Page 182-195; 246pp; English.

CC The present invention relates to a method of identifying a compound  
CC that modulates attention deficit hyperactivity disorder (ADHD) in  
CC a mammal. The method comprises administering a test compound to  
CC an invertebrate, and measuring a foraging behaviour of the  
CC invertebrate, where the compound that modulates the foraging behaviour  
CC of the invertebrate is characterised as a compound that modulates  
CC ADHD in a mammal. The compound identified by the new method of the  
CC invention is useful for diagnosing or treating ADHD, hypertension or  
CC other diseases associated with a nitric oxide/GMP-dependent protein  
CC kinase network in a mammal, particularly humans. The method  
CC distinguishes a compound that has a specific effect on ADHD,  
CC hypertension or other diseases associated with a  
CC nitric oxide/GMP-dependent kinase protein network  
CC in a mammal from a compound that has a non-specific effect. The  
CC present sequence represents a DNA sequence associated with  
CC invertebrate foraging behaviour.

SQ Sequence 42999 BP; 6411 A; 13605 C; 11491 G; 11479 T; 13 other;

Query Match 15.2%; Score 38.4; DB 24; Length 42999;  
Best Local Similarity 48.4%; Pred. No. 11;

Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 1 CCGCGCGGAGGCGCGCGGAGTGAGGCTGATGTCCTTGCGCTCCACTCCCGCAG 60  
DB 7676 CCGCGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7617  
QY 61 CGCAGAGAGGCG 120  
DB 7616 GCG 7557  
QY 121 CAGGAGACAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
DB 7556 TCGCCG 7497  
QY 181 CCCTCAGCAGGAGGAGCTCCCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCG 217  
DB 7496 CCG 7460

RESULT 13  
AAF30761/C  
ID AAF30761 standard; DNA; 528 BP.

AC AAF30761;  
XX  
DT 21-JUN-2001 (first entry)  
XX  
DE Megalomycin polyketide synthase codon engineered module 6.  
XX  
KW Megalomycin; meg gene; polyketide synthase; antibiotic;  
KW motillide; antiparasitic; mutant; de.  
XX  
OS Micromonospora megalomicea subsp. nigra.  
XX  
PN WO200127284-A2.  
XX  
PD 19-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US27433.  
XX  
PR 08-OCT-1999; 99US-0158305.  
PR 17-MAR-2000; 2000US-0190024.  
XX  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
XX  
PI McDaniel R, Volchegursky Y;  
XX  
DR WPI; 2001-282034/29.

PT Nucleic acids encoding a domain of megalomycin polyketide synthase or a  
PT megalomycin modification enzyme, useful for the production of  
PT megalomycin for use as antibiotics, motillides and antiparasitics -  
XX  
XX  
PS Example 2; Page 99; 189pp; English.

CC The present sequence of that of bases 26736-27267 in a codon  
CC engineered module 6 of the Micromonospora megalomicea subsp. nigra  
CC ATCC 27587 (NRRL3275) megalomycin polyketide synthase (PKS) gene  
CC cluster (see AAF30757). Expression plasmids containing the  
CC full-length megalomycin PKS were unstable and subject to deletion  
CC in recA+ strains. To prevent homologous recombination and so  
CC stabilize the plasmids, the codons of 2 regions of the module 6  
CC coding sequence that are identical to regions in module 2 of protein  
CC encoded. The 2 regions changed in module 6 were bases 26739-27267  
CC (see AAF30760) and 27697-27987 (see AAF30763), which were identical  
CC to module 2 bases 6810-7338 (see AAF30759) and 7778-8068,  
CC respectively. The start codon of the loading domain of the meg PKS  
CC was set as the first base. Codon engineering of module 6  
CC stabilized meg PKS expression in bacterial host cells. The  
CC invention provides nucleic acids encoding all or a portion of  
CC the megalomycin PKS and modification enzymes, which can be used to







PT antisense sequences of granule bound synthase  
XX  
PS Claim 17, Page 63-65; 171pp; English.  
XX  
CC The invention relates to a novel enzyme of starch biosynthetic pathway  
CC in a cereal plant, where the enzyme is selected from starch branching  
CC enzyme (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching  
CC enzyme (DBE), with the proviso that the enzyme is not SSS I of rice, or  
CC SBE I of rice or maize. The methods and products can be used for  
CC targeting expression specifically to the endosperm of the seeds of cereal  
CC plants such as wheat or barley. They can be used for the expression of  
CC 6 g. antisense sequences of granule-bound synthase (GBS), SBE II, low  
CC mol. wt. glutelin, grain softness protein 1, bacterial isomylase,  
CC bacterial glycogen synthase, and wheat high mol. wt. glutelin Bx17. They  
CC can be used for modifying the characteristics of starch produced by a  
CC plant. The present sequence represents the wheat SBE I promoter  
CC containing sequence.  
XX  
SQ Sequence 4890 BP; 1403 A; 1067 C; 1035 G; 1385 T; 0 other;  
Query Match 15.1%; Score 38; DB 20; Length 4890;  
Best Local Similarity 51.5%; Pred. No. 14;  
Matches 86; Conservative 0; Mismatches 81; Indels 0; Gaps 0;  
OY 24 GAGGCTGATCTCTCTGCGCTCCACCTCCCGACGCGCAGAGGCGCCCAAGAGCC 83  
DB 173 GGGCCCTGTCTCGACCCGAGACCTCAGCTGCGCGGCTTTAAAGCCGACGCTGCGCC 114  
OY 84 CCCAGTGGCCGACGTTGCCACGCGTGGAGATCAGAGGACCGACGAGGCGCAGAACT 143  
DB 113 CGCTCAGGCGCAAGTGGCGCGCGCGCGGAAACCTTAGCGCGCTGCGCGCGCGCG 54  
OY 144 GGGCGCGCGCGCGCGCGCGCTGCGCGCGCGGAGGAGCTCCTCAGCNG 190  
DB 53 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTGGCGCGCGACCGG 7  
RESULT 18  
ABX9879  
ID ABX9879 standard; cDNA; 1947 BP.  
XX  
AC ABX9879;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human cDNA encoding a novel kinase protein #6.  
XX  
KW Human; ss; kinase; gene; noctropic; gene therapy; novel human protein;  
KW NHP; serine-threonine kinase; casein kinase; mitogen activated kinase;  
KW calcium/calmodulin-dependent protein kinase; chromosome 6;  
KW mental disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200248333-A2.  
XX  
PD 20-JUN-2002.  
XX  
PF 12-DEC-2001; 2001WO-US49068.  
XX  
PR 12-DEC-2000; 2000US-25103P.  
PR 08-MAY-2001; 2001US-289422P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Turner CA, Mathur B, Friddle CJ;  
XX  
DR WPI, 2002-583505/62.  
DR P-PDB; ABG69455.  
XX  
XX Novel polynucleotides encoding human proteins that are structurally  
PT related to animal kinases, useful for drug screening, diagnosis and in  
PT gene therapy of biological disorders

XX  
XX Disclosure; Page 50-51; 94pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule comprising a  
CC nucleotide sequence encoding a novel human protein (NHP) appearing  
CC as ABG69450-ABG69469, that share structural similarity with animal  
CC kinases, including serine-threonine kinases, casein kinases,  
CC calcium/calmodulin-dependent protein kinases and mitogen activated  
CC kinases. NHP oligonucleotides are useful as hybridization probes for  
CC screening libraries and assessing gene expression patterns. NHP  
CC sequences are useful to identify mutations associated with a particular  
CC disease and also as a diagnostic or prognostic assay, and also in the  
CC molecular mutagenesis/evolution of proteins that are at least partially  
CC encoded by the NHP boundaries. Sequences derived from regions adjacent  
CC to the intron/exon boundaries of NHP gene can be used to design primers  
CC for use in amplification assays to detect mutations within the exons,  
CC splice sites, introns that can be used in diagnostics and  
CC pharmacogenomics. NHP sequences are utilized in microarrays or other  
CC assay formats, to screen collections of genetic material from patients  
CC who have a particular medical condition. NHP nucleotide sequences are  
CC useful for drug screening effective in the treatment of symptomatic or  
CC phenotypic manifestations of perturbing the normal function of NHP in the  
CC body, and nucleotide constructs encoding NHP products are used to  
CC genetically engineer host cells to express NHP products in vivo. These  
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
CC protein to the body. Nucleotide constructs encoding NHP products are also  
CC useful in gene therapy for modulating NHP expression. The encoded NHP  
CC polypeptides are useful for generating antibodies, as reagents in  
CC diagnostic assays, for identifying other cellular gene products related  
CC to NHP and as reagents in assays for screening for compounds that are  
CC useful in the treatment of mental, biological or medical disorders and  
CC diseases. The gene for the NHP is located on human chromosome 6.  
XX  
SQ The present sequence encodes an NHP of the invention.  
XX  
SQ Sequence 1947 BP; 395 A; 586 C; 658 G; 306 T; 2 other;  
Query Match 15.0%; Score 37.8; DB 24; Length 1947;  
Best Local Similarity 50.6%; Pred. No. 16;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
OY 35 GTCCCTGGCGCTTCCACCTTCCCGAGAGGCGCCCGACGAGAGCCCGGCGCCG 94  
DB 41 GCGCGTGGCGCGCGCGCGCGCGCGAGAGATCGGGCGCGCGCGCGAGATGATCGG 100  
OY 95 ACGTTGACAGGCTGTGGATCAGAGGACGAGGACGAGAGCCAGAGACTGCGCGCCG 154  
DB 101 GTCGAGAGGCGCGCGCGCGCGCGAGGAGCGGGGTACCCAAAGCGGACGTGAGCGCCCG 160  
OY 155 GCGCGTGGCGCGAGGAGAGTCCCTCACCAGAGGAGAGTCCCTCAGCCCGCGC 212  
DB 161 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGCTGCTGCGCGCGCGCGC 218  
RESULT 19  
ABX90541  
ID ABX90541 standard; cDNA; 1947 BP.  
XX  
AC ABX90541;  
XX  
DT 02-MAY-2003 (first entry)  
XX  
DE Human kinase cDNA #6.  
XX  
KW Human; gene; ss; kinase; phosphorylation; regulatory pathway;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2002161213-A1.  
XX  
PD 31-OCT-2002.

PF 12-DEC-2001; 2001US-0020079.  
XX  
PR 12-DEC-2000; 2000US-255103P.  
XX 08-MAY-2001; 2001US-289422P.  
XX  
PA (TURN/) TURNER C A.  
PA (MATH/) MATHUR B.  
PA (FRID/) FRIDDLE C J.  
XX  
PI Turner CA, Mathur B, Friddle CJ;  
XX WPI; 2003-288125/28.  
DR P-PSDB; ABU60660.  
XX  
PT New novel human polynucleotides encoding proteins sharing sequence  
PT similarity with animal kinases, useful for diagnosing or treating  
PT disorders -  
XX  
PS Disclosure; Page 26-27; 78pp; English.

CC The invention discloses isolated nucleic acids, and the protein that they  
CC encode, of novel human kinases. Kinases mediate the phosphorylation of a  
CC wide variety of proteins and compounds in the cell and are involved in a  
CC range of regulatory pathways. The novel human polynucleotides, encoding  
CC proteins sharing sequence similarity with animal kinases, are useful for  
CC diagnosing or treating (e.g. gene therapy) disorders. The sequence  
CC presented is a cDNA encoding a human kinase.

SO Sequence 1947 BP; 395 A; 586 C; 658 G; 306 T; 2 other;

Query Match 15.0%; Score 37.8; DB 25; Length 1947;  
Best Local Similarity 50.6%; Pred. No. 16;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

OY 35 GTCCTGCGCGCTCCACCTCCCGAGCGAGAGCGGCCACGAGACCCCGAGTCCCG 94  
DB 41 GCGGCTGCGCGCGCTCCCGAGAGATCGGGCCGCGCGCGCGAGTGTATCCGG 100  
OY 95 ACCTTGCCACGCTGTGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 154  
DB 101 GTCCGAAGCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 160  
OY 155 GCGGCTGCGCGCGCGAG 212  
DB 161 GCGGCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 218

RESULT 20

ABK99878  
ID ABK99878 standard; cDNA; 1965 BP.

AC ABK99878;

DT 21-OCT-2002 (first entry)

XX Human cDNA encoding a novel kinase protein #5.

XX Human; ss; kinase; gene; noctropic; gene therapy; novel human protein;  
XX NHP; serine-threonine kinase; casein kinase; mitogen activated kinase;  
XX calcium/calmodulin-dependent protein kinase; chromosome 6; SNP;  
XX mental disorder; single nucleotide polymorphism.

OS Homo sapiens.

XX  
XX Key Location/Qualifiers  
XX variation /tag a  
XX /standard\_name= "Single nucleotide polymorphism"

PN MO200248333-A2.

PD 20-JUN-2002.

PF 12-DEC-2001; 2001US-0020079.  
XX  
PR 12-DEC-2000; 2000US-255103P.  
XX 08-MAY-2001; 2001US-289422P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Turner CA, Mathur B, Friddle CJ;  
XX WPI; 2002-583505/62.  
DR P-PSDB; ABG69454.  
XX  
PT Novel polynucleotides encoding human proteins that are structurally  
PT related to animal kinases, useful for drug screening, diagnosis and in  
PT gene therapy of biological disorders -  
XX  
PS Disclosure; Page 48; 94pp; English.

CC The invention relates to an isolated nucleic acid molecule comprising a  
CC nucleotide sequence encoding a novel human protein (NHP) appearing  
CC as ABG69450-ABG69469, that share structural similarity with animal  
CC kinases, including serine-threonine kinases, casein kinases,  
CC calcium/calmodulin-dependent protein kinases, and mitogen activated  
CC kinases. NHP oligonucleotides are useful as hybridization probes for  
CC screening libraries and assessing gene expression patterns. NHP  
CC sequences are useful to identify mutations associated with a particular  
CC disease and also as a diagnostic or prognostic assay, and also in the  
CC molecular mutagenesis/evolution of proteins that are at least partially  
CC encoded by the NHP sequences. Sequences derived from regions adjacent  
CC to the intron/exon boundaries of NHP gene can be used to design primers  
CC for use in amplification assays to detect mutations within the exons,  
CC splice sites, introns that can be used in diagnostics and  
CC pharmacogenomics. NHP sequences are utilized in microarrays or other  
CC assay formats, to screen collections of genetic material from patients  
CC who have a particular medical condition. NHP nucleotide sequences are  
CC useful for drug screening effective in the treatment of symptomatic or  
CC phenotypic manifestations of perturbing the normal function of NHP in the  
CC body, and nucleotide constructs encoding NHP products are used to  
CC genetically engineer host cells to express NHP products in vivo. These  
CC genetically engineered cells function as bioreactors in the body  
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
CC protein to the body. Nucleotide constructs encoding NHP products are also  
CC useful in gene therapy for modulating NHP expression. The encoded NHP  
CC polypeptides are useful for generating antibodies, as reagents in  
CC diagnostic assays, for identifying other cellular gene products related  
CC to NHP and as reagents in assays for screening for compounds that are  
CC useful in the treatment of NHP related, biological or medical disorders and  
CC diseases. The gene for the NHPs is located on human chromosome 6.  
CC The present sequence encodes an NHP of the invention.

SO Sequence 1965 BP; 397 A; 589 C; 666 G; 311 T; 2 other;

Query Match 15.0%; Score 37.8; DB 24; Length 1965;  
Best Local Similarity 50.6%; Pred. No. 16;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

OY 35 GTCCTGCGCGCTCCACCTCCCGAGCGAGAGCGGCCACGAGACCCCGAGTCCCG 94  
DB 59 GCGGCTGCGCGCGCTCCCGAGAGATCGGGCCGCGCGCGCGAGTGTATCCGG 118  
OY 95 ACCTTGCCACGCTGTGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 154  
DB 119 GTCCGAAGCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 178  
OY 155 GCGGCTGCGCGCGAG 212  
DB 179 GCGGCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 236

RESULT 21

ABX90540  
ID ABX90540 standard; cDNA; 1965 BP.

AC ABX90540;  
 XX 02-MAY-2003 (first entry)  
 XX Human kinase cDNA #5.  
 XX Human kinase cDNA #5.  
 XX Human, gene; ss; kinase; phosphorylation; regulatory pathway;  
 XX gene therapy.  
 XX Homo sapiens.  
 OS  
 PN US2002161213-A1.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 12-DEC-2001; 2001US-0020079.  
 XX  
 PR 12-DEC-2000; 2000US-255103P.  
 PR 08-MAY-2001; 2001US-289422P.  
 XX  
 PA (TURN/) TURNER C A.  
 PA (MATH/) MATHUR B.  
 PA (FRID/) FRIDDLE C J.  
 XX  
 PI Turner CA, Mathur B, Friddle CJ;  
 XX  
 DR WPI; 2003-288125/28.  
 DR P-PSDB; ABU60559.  
 XX  
 PT New novel human polynucleotides encoding proteins sharing sequence  
 PT similarity with animal kinases, useful for diagnosing or treating  
 PT disorders -  
 XX  
 PS Disclosure; Page 23-24; 78pp; English.  
 XX  
 CC The invention discloses isolated nucleic acids, and the protein that they  
 CC encode, of novel human kinases. Kinases mediate the phosphorylation of a  
 CC wide variety of proteins and compounds in the cell and are involved in a  
 CC range of regulatory pathways. The novel human polynucleotides, encoding  
 CC proteins sharing sequence similarity with animal kinases, are useful for  
 CC diagnosing or treating (e.g. gene therapy) disorders. The sequence  
 CC presented is a cDNA encoding a human kinase.  
 CC  
 CC Sequence 1965 BP; 397 A; 589 C; 666 G; 311 T; 2 other;  
 CC  
 CC Query Match 15.0%; Score 37.8; DB 25; Length 1965;  
 CC Best Local Similarity 50.6%; Pred. No. 16;  
 CC Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
 CC  
 CC  
 CC 35 GTCCTGCGCGCTCCCACTCCCGAGGCGCGAGAGCGCCCGCCAGTGCCTCG 94  
 CC 59 GCGCGTGCCTGCGCGCTCCCGAGGCGCGAGAGCGCGCGCGCGCGATGATCCG 118  
 CC 95 AGCTGCGCGCGCTGCGCGATCAGAGGCGCGAGGCGCGAGAGCGCGCGCGCGCG 154  
 CC 119 GTCGGAAGCGCGCGCGCGCGCGAGGAGCGCGGTCAACCGCGCGCGCGCGCGCG 178  
 CC 155 GCG 212  
 CC 179 GCG 236  
 CC  
 CC RESULT 22  
 CC AAD30551  
 CC ID AAD30551 standard; cDNA; 2341 BP.  
 CC  
 CC AAD30551;  
 CC  
 CC 21-MAY-2002 (first entry)  
 CC  
 CC Human kinase polypeptide (PKIN-4) cDNA.  
 CC  
 CC Human; kinase polypeptide; PKIN-4; gene therapy; Addison's disease;

KW Leukaemia; immune disorder; lymphoma; melanoma; developmental disorder;  
 KW acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension;  
 KW asthma; Crohn's disease; rheumatoid arthritis; buritis; atherosclerosis;  
 KW cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer;  
 KW cholestasis; cardiac; cardiovascular disorder; Niemann-Pick's disease;  
 KW lipid disorder; fatty liver; Gaucher's disease; myocardial infarction;  
 KW drug screening; transgenic animal; antiinflammatory; hepatotropic;  
 KW hypotensive; anti-HIV; enzyme; ss.  
 XX  
 OS  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2226  
 FT /tag=a  
 FT /product="Human PKIN-4"  
 FT sig\_peptide 1..57  
 FT /tag=b  
 FT mat\_peptide 58..2223  
 FT /tag=c  
 FT /product="Mature human PKIN-4"  
 XX  
 PN WO200208399-A2.  
 XX  
 PD 31-JAN-2002.  
 XX  
 PF 20-JUL-2001; 2001WO-US23092.  
 XX  
 PR 21-JUL-2000; 2000US-220038P.  
 PR 28-JUL-2000; 2000US-222112P.  
 PR 04-AUG-2000; 2000US-222831P.  
 PR 11-AUG-2000; 2000US-224729P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 PA (THOR/) THORNTON M.  
 XX  
 PI Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Walla NK;  
 PI Patterson C, Rakhumai J, Gandhi AR, Policky JL, Baughn MK;  
 PI Tribolety CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lai P;  
 PI Ding L, Yao MG, Elliott VS, Reardon SA, Kearney L, Lu DM;  
 PI Greenwald SR, Tang YT, Xu Y, Walsh RT, Gietzen KU, Yang J;  
 PI Hillman JL;  
 XX  
 DR WPI; 2002-206083/26.  
 DR P-PSDB; AAE19146.  
 XX  
 PT New human kinase polypeptide, useful in diagnosis, prevention and  
 PT treatment of cancer, immune disorder, growth and developmental  
 PT disorder, cardiovascular disorder and lipid disorder -  
 XX  
 PS Claim 5; Page 177-178; 196pp; English.  
 XX  
 CC The present invention relates to an isolated human kinase polypeptide  
 CC (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is  
 CC useful for diagnosing, treating and preventing cancer (e.g., leukaemia,  
 CC lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency  
 CC syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's  
 CC disease, rheumatoid arthritis), a growth and developmental disorder (e.g.,  
 CC buritis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a  
 CC cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial  
 CC infarction), and a lipid disorder (e.g., fatty liver, cholestasis,  
 CC Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of  
 CC drug screening techniques and to analyse the proteome of a tissue or cell  
 CC type. PKIN is useful for creating knockin humanised animals or transgenic  
 CC animals to model human diseases, in somatic or germ-line gene therapy, to  
 CC generate a transcript image of a tissue or cell type, for detecting  
 CC differences in the chromosomal location due to translocation, inversion,  
 CC etc., among normal, carrier or affected individuals, and as hybridisation  
 CC probes for mapping naturally occurring genomic sequences. PKIN is useful  
 CC in southern or northern analysis, dot blot or other membrane-based  
 CC technologies, in PCR technologies, in dipstick, pin, microarray enzyme  
 CC linked immunosorbent (ELISA)-like assays and in microarrays utilising  
 CC fluids or tissues from patients to detect altered PKIN expression. The  
 CC present sequence is human PKIN-4 cDNA.

XX SQ Sequence 2341 BP, 447 A, 724 C, 770 G, 400 T, 0 other;  
Query Match 15.0%; Score 37.8; DB 24; Length 2341;  
Best Local Similarity 50.6%; Pred. No. 16;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
DB 35 GTCCCTGGCGCTCCACCTCCCGCAGAGGCGCCCAAGAGACCCCGAGGCGCG 94  
59 GCCCTGCGCGCGCTCCCGCCCAAGAGATCGGGCGCGCGCGCGCGGATATCCGG 118  
QY 95 ACGTTGCCACGCTCTGGATCAGAGGCGAGGAGCCAGAGACTGCGCGCGCGCG 154  
DB 119 GTCCGAAAGCGCGCGCGCGCGAGGAGCGGATCACCAGCGCGCACTAGCGCGCG 178  
QY 155 GCCCTGCGCGCTGGCGCGGAGAGTCTCTCAACGAGGAGAACTCCCTTACCGCGC 212  
DB 179 GCCCGCGCGCGCGCGCGGAGATGCGCGCGCGCGCGCGCTGCTCGCGCGCGCGC 236  
RESULT 23  
ABK9875  
ID ABK9875 standard; cDNA, 2595 BP.  
XX AC ABK9875;  
XX DT 21-OCT-2002 (first entry)  
XX DE Human cDNA encoding a novel kinase protein #2.  
XX KW Human; ss; kinase; gene; neotropic; gene therapy; novel human protein;  
KW NHP; serine-threonine kinase; casein kinase; mitogen activated kinase;  
KW calcium/calmodulin-dependent protein kinase; chromosome 6;  
KW mental disorder.  
XX OS Homo sapiens.  
XX PN WO200248333-A2.  
XX PD 20-JUN-2002.  
XX PF 12-DEC-2001; 2001WO-US49068.  
XX PR 12-DEC-2000; 2000US-255103P.  
XX PR 08-MAY-2001; 2001US-289422P.  
XX PA (LEXI-) LEXICON GENETICS INC.  
XX PI Turner CA, Mathur B, Fiddle CJ;  
XX DR WPI; 2002-583505/62.  
XX DR P-PSDB; ABG69451.  
XX PT Novel polynucleotides encoding human proteins that are structurally  
PT related to animal kinases, useful for drug screening, diagnosis and in  
PT gene therapy of biological disorders  
XX PS Disclosure; Page 39-40; 94pp; English.  
XX CC The invention relates to an isolated nucleic acid molecule comprising a  
CC nucleotide sequence encoding a novel human protein (NHP) appearing  
CC as ABG69450-ABG69469, that share structural similarity with animal  
CC kinases, including serine-threonine kinases, casein kinases,  
CC calcium/calmodulin-dependent protein kinases, and mitogen activated  
CC kinases. NHP oligonucleotides are useful as hybridisation probes for  
CC screening libraries and assessing gene expression patterns. NHP  
CC sequences are useful to identify mutations associated with a particular  
CC disease and also as a diagnostic or prognostic assay, and also in the  
CC molecular mutagenesis/evolution of proteins that are at least partially  
CC encoded by the NHP sequences. Sequences derived from regions adjacent  
CC to the intron/exon boundaries of NHP gene can be used to design primers  
CC for use in amplification assays to detect mutations within the exons,  
CC splice sites, introns that can be used in diagnostics and

CC pharmacogenomics. NHP sequences are utilised in microarrays or other  
CC assay formats, to screen collections of genetic material from patients  
CC who have a particular medical condition. NHP nucleotide sequences are  
CC useful for drug screening effective in the treatment of symptomatic or  
CC phenotypic manifestations of perturbing the normal function of NHP in the  
CC body, and nucleotide constructs encoding NHP products are used to  
CC genetically engineer host cells to express NHP products in vivo. These  
CC genetically engineered cells function as bioreactors in the body  
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
CC protein to the body. Nucleotide constructs encoding NHP products are also  
CC useful in gene therapy for modulating NHP expression. The encoded NHP  
CC polypeptides are useful for generating antibodies, as reagents in  
CC diagnostic assays, for identifying other cellular gene products related  
CC to NHP and as reagents in assays for screening for compounds that are  
CC useful in the treatment of mental biological or medical disorders and  
CC diseases. The gene for the NHPs is located on human chromosome 6.  
XX CC The present sequence encodes an NHP of the invention.  
XX SQ Sequence 2595 BP, 498 A, 865 C, 845 G, 385 T, 2 other;  
Query Match 15.0%; Score 37.8; DB 24; Length 2595;  
Best Local Similarity 50.6%; Pred. No. 16;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
DB 35 GTCCCTGGCGCTCCACCTCCCGCAGAGGCGCCCAAGAGACCCCGAGTGC 94  
41 GCCGCTGCGCGCGCGCTCCCGCCCAAGAGGATCGGGCGCGCGCGCGGATATCCGG 100  
QY 95 ACGTTGCCACGCTCTGGATCAGAGGCGAGGAGCCAGAGAACTGCGCGCGCGCG 154  
DB 101 GTCCGAAAGCGCGCGCGCGCGGAGGAGCGGATCACCAGCCGCACTGAGCGCGCG 160  
QY 155 GCCCTGCGCGCTGGCGCGGAGAGTCTCTCAACGAGGAGAACTCCCTTACCGCGC 212  
DB 161 GCCCGCGCGCGCGCGCGGAGATGCGCGCGCGCGCGCGCTGCTCGCGCGCGCGC 218  
RESULT 24  
ABK90537  
ID ABK90537 standard; cDNA, 2595 BP.  
XX AC ABK90537;  
XX DT 02-MAY-2003 (first entry)  
XX DE Human kinase cDNA #2.  
XX KW Human; gene; ss; kinase; phosphorylation; regulatory pathway;  
KW gene therapy.  
XX OS Homo sapiens.  
XX PN US2002161213-A1.  
XX PD 31-OCT-2002.  
XX PF 12-DEC-2001; 2001US-0020079.  
XX PR 12-DEC-2000; 2000US-255103P.  
XX PR 08-MAY-2001; 2001US-289422P.  
XX PA (TURN/) TURNER C A.  
XX PA (MATH/) MATHUR B.  
XX PA (FRID/) FRIDDLE C J.  
XX PI Turner CA, Mathur B, Fiddle CJ;  
XX DR WPI; 2003-286125/28.  
XX DR P-PSDB; ABU60656.  
XX PT New novel human polynucleotides encoding proteins sharing sequence  
PT similarity with animal kinases, useful for diagnosing or treating  
PT disorders



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XX 31-OCT-2002.
PD 12-DEC-2001; 2001US-0020079.
XX
XX 12-DEC-2001; 2001US-289422P.
XX
XX 12-DEC-2001; 2001US-289422P.
XX
XX 08-MAY-2001; 2001US-289422P.
XX
XX (TURNER) TURNER C A.
XX (MATH) MATHUR B.
XX (FRID) FRIDDLE C J.
XX
XX Turner CA, Mathur B, Friddle CJ;
XX
XX WPI; 2003-288125/28.
XX P-PSDB; AB060655.
XX
XX New novel human polynucleotides encoding proteins sharing sequence
XX similarity with animal kinases, useful for diagnosing or treating
XX disorders -
XX
XX Claim 2; Page 9-11; 78bp; English.
XX
XX The invention discloses isolated nucleic acids, and the protein that they
XX encode, of novel human kinases. Kinases mediate the phosphorylation of a
XX wide variety of proteins and compounds in the cell and are involved in a
XX range of regulatory pathways. The novel human polynucleotides, encoding a
XX proteins sharing sequence similarity with animal kinases, are useful for
XX diagnosing or treating (e.g. gene therapy) disorders. The sequence
XX presented is a cDNA encoding a human kinase, the gene for which is
XX located on chromosome 6.
XX
XX Sequence 2613 BP; 500 A; 868 C; 853 G; 390 T; 2 other;
XX
XX Query Match 15.0%; Score 37.8; DB 25; Length 2613;
XX Best Local Similarity 50.6%; Pred. No. 16;
XX Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
XX
XX QY 35 GTCCCTGGGCGCTTCACCTCCCGAGGCGCCACGAGAGACCCCACTGCCCCG 94
XX Db 59 GCGCGTGGCGCGCGCTTCGCGCCAGAGAGATCGGGCGCGCGCGGATGATCCGG 118
XX QY 95 ACCTTCCACGCTGTGATCAAGAGCAGGACCGAGGACCAAGAACTGCCCCCCCC 154
XX Db 119 GTCGGAAGGCGCGCGCGCGCGAGGAGCGGTCAACCGCCGACTGAGCCGCCCCC 178
XX QY 155 GCGCCCTGCGCTGCGCGAGGAGAACTCCCTCAACGAGGAAAGTCCCTCAACCGCGC 212
XX Db 179 GCGCCGCGCGCGCGCGCGGAGATGCGCCCGCCCGAGCTGCTCGCGCGCGCGCGC 236
XX
XX RESULT 27
XX ABR9883
XX ID ABR9883 standard; cDNA; 2670 BP.
XX
XX ABR9883;
XX
XX DT 21-OCT-2002 (first entry)
XX
XX Human cDNA encoding a novel kinase protein #10.
XX
XX Human; ser. kinase; gene; noctropic; gene therapy; novel human protein;
XX NHP; serine-threonine kinase; casein kinase; mitogen activated kinase;
XX calcium/calmodulin-dependent protein kinase; chromosome 6;
XX mental disorder.
XX
XX Homo sapiens.
XX
XX WO200248333-A2.
XX
XX 20-JUN-2002.
XX
XX 12-DEC-2001; 2001WO-US49068.
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XX 12-DEC-2001; 2001US-289422P.
XX
XX 08-MAY-2001; 2001US-289422P.
XX
XX (LEXT-) LEXICON GENETICS INC.
XX
XX Turner CA, Mathur B, Friddle CJ;
XX
XX WPI; 2002-583505/62.
XX P-PSDB; AB069459.
XX
XX Novel polynucleotides encoding human proteins that are structurally
XX related to animal kinases, useful for drug screening, diagnosis and in
XX gene therapy of biological disorders -
XX
XX Disclosure; Page 60-61; 94bp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising a
XX nucleotide sequence encoding a novel human protein (NHP) appearing
XX as AB069450-AB069469, that share structural similarity with animal
XX kinases, including serine-threonine kinases, casein kinases,
XX calcium/calmodulin-dependent protein kinases and mitogen activated
XX kinases. NHP oligonucleotides are useful as hybridisation probes for
XX screening libraries and assessing gene expression patterns. NHP
XX sequences are useful to identify mutations associated with a particular
XX disease and also as a diagnostic or prognostic assay, and also in the
XX molecular mutagenesis/evolution of proteins that are at least partially
XX encoded by the NHP sequences. Sequences derived from regions adjacent
XX to the intron/exon boundaries of NHP gene can be used to design primers
XX for use in amplification assays to detect mutations within the exons,
XX splice sites, introns that can be used in diagnostics and
XX pharmacogenomics. NHP sequences are utilised in microarrays or other
XX assay formats, to screen collections of genetic material from patients
XX who have a particular medical condition. NHP nucleotide sequences are
XX useful for drug screening effective in the treatment of symptomatic or
XX phenotypic manifestations of perturbing the normal function of NHP in the
XX body, and nucleotide constructs encoding NHP products are used to
XX genetically engineer host cells to express NHP products in vivo. These
XX constructs are useful for screening and identifying NHP products that
XX deliver a continuous supply of a NHP, a NHP peptide, or a NHP fusion
XX protein to the body. Nucleotide constructs encoding NHP products are also
XX useful in gene therapy for mediating NHP expression. The encoded NHP
XX polypeptides are useful for generating antibodies, as reagents in
XX diagnostic assays, for identifying other cellular gene products related
XX to NHP and as reagents in assays for screening for compounds that are
XX useful in the treatment of mental, biological or medical disorders and
XX diseases. The gene for the NHP is located on human chromosome 6.
XX
XX The present sequence encodes an NHP from the invention.
XX
XX Sequence 2670 BP; 538 A; 846 C; 863 G; 421 T; 2 other;
XX
XX Query Match 15.0%; Score 37.8; DB 24; Length 2670;
XX Best Local Similarity 50.6%; Pred. No. 16;
XX Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
XX
XX QY 35 GTCCCTGGGCGCTTCACCTCCCGAGGCGCCACGAGAGACCCCACTGCCCCG 94
XX Db 41 GCGCGTGGCGCGCGCTTCGCGCCAGAGAGATCGGGCGCGCGCGGATGATCCGG 100
XX QY 95 ACCTTCCACGCTGTGATCAAGAGCAGGACCGAGGACCAAGAACTGCCCCCCCC 154
XX Db 101 GTCGGAAGGCGCGCGCGCGCGAGGAGCGGTCAACCGCCGACTGAGCCGCCCCC 160
XX QY 155 GCGCCCTGCGCTGCGCGAGGAGAACTCCCTCAACGAGGAAAGTCCCTCAACCGCGC 212
XX Db 161 GCGCCGCGCGCGCGCGCGGAGATGCGCCCGCCCGAGCTGCTCGCGCGCGCGC 218
XX
XX RESULT 28
XX ABR90545
XX ID ABR90545 standard; cDNA; 2670 BP.
XX
XX ABR90545;
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XX 02-MAY-2003 (first entry)  
 DT Human kinase cDNA #10.  
 XX Human; gene; sr; kinase; phosphorylation; regulatory pathway;  
 KW gene therapy.  
 XX Homo sapiens.  
 OS US2002161213-A1.  
 PN 31-OCT-2002.  
 XX 12-DEC-2001; 2001US-0020079.  
 PF 12-DEC-2000; 2000US-255103P.  
 PR 08-MAY-2001; 2001US-289422P.  
 XX (TURN/) TURNER C A.  
 PA (MATH/) MATHUR B.  
 PI (FRID/) FRIDDLE C J.  
 XX Turner CA, Mathur B, Friddle CJ;  
 PI WPI; 2003-288125/28.  
 DR P-PSDB; AB060664.  
 XX New novel human polynucleotides encoding proteins sharing sequence  
 PT similarity with animal kinases, useful for diagnosing or creating  
 PT disorders -  
 PS Disclosure; Page 37-38; 78pp; English.  
 XX The invention discloses isolated nucleic acids, and the protein that they  
 CC encode, of novel human kinases. Kinases mediate the phosphorylation of a  
 CC wide variety of proteins and compounds in the cell and are involved in a  
 CC range of regulatory pathways. The novel human polynucleotides, encoding  
 CC proteins sharing sequence similarity with animal kinases, are useful for  
 CC diagnosing or treating (e.g. gene therapy) disorders. The sequence  
 CC presented is a cDNA encoding a human kinase.  
 XX Sequence 2670 BP; 538 A; 846 C; 863 G; 421 T; 2 other;  
 SQ  
 Query Match 15.0%; Score 37.8; DB 25; Length 2670;  
 Best Local Similarity 50.6%; Pred. No. 16;  
 Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
 QY 35 GTCCTGCGCGCTCCCACTCCCGAGGCGCCGAGAGGCGCCCGAGGAGCCCGAGTGCCTCG 94  
 Db 41 GCGCGTCCCGCGCGCGCTCCCGAGGAGATCGGGCGCGCGCGCGCGAGTGCCTCG 100  
 QY 95 ACGTTGCCACGCTGTGGATCAAGAGCGAGGAGCCAGAGGAGCCAGAACTGCGCGCGCGCG 154  
 Db 101 GTCGGAAGCGCGCGCGCGCGCGAGGAGCGGATCAAGAGCGCGCGAGTGCCTCGCGCGCG 160  
 QY 155 GCCCGTCCCGCGCGCGAGGAGGAGTCCCTCACGAGGAGGAGTCCCTCGAGCGCGCGCG 212  
 Db 161 GCCCGCGCGCGCGCGCGCGAGGAGTGCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 218

RESULT 29  
 ABK9882  
 ID ABK9882 standard; cDNA; 2688 BP.  
 XX  
 AC ABK9882;  
 DT 21-OCT-2002 (first entry)  
 XX Human cDNA encoding a novel kinase protein #9.  
 DE Human; sr; kinase; gene; neotropic; gene therapy; novel human protein;  
 KW NHP; serine-threonine kinase; casein kinase; mitogen activated kinase;

KW calcium/calmodulin-dependent protein kinase; chromosome 6;  
 KM mental disorder.  
 XX Homo sapiens.  
 OS WO200248313-A2.  
 XX 20-JUN-2002.  
 XX 12-DEC-2001; 2001WO-US49068.  
 PF 12-DEC-2000; 2000US-255103P.  
 PR 08-MAY-2001; 2001US-289422P.  
 XX (LEXI-) LEXICON GENETICS INC.  
 PA Turner CA, Mathur B, Friddle CJ;  
 PI WPI; 2002-583505/62.  
 DR P-PSDB; ABG69458.  
 XX Novel polynucleotides encoding human proteins that are structurally  
 PT related to animal kinases, useful for drug screening, diagnosis and in  
 PT gene therapy of biological disorders -  
 PS Disclosure; Page 57; 94pp; English.  
 XX The invention relates to an isolated nucleic acid molecule comprising a  
 CC nucleotide sequence encoding a novel human protein (NHP) appearing  
 CC as ABG69450-ABG69469, that share structural similarity with animal  
 CC kinases, including serine-threonine kinases, casein kinases,  
 CC calcium/calmodulin-dependent protein kinases, and mitogen activated  
 CC kinases. NHP oligonucleotides are useful as hybridization probes for  
 CC screening libraries and assessing gene expression patterns. NHP  
 CC sequences are useful to identify mutations associated with a particular  
 CC disease and also as a diagnostic or prognostic assay, and also in the  
 CC molecular mutagenesis/evolution of proteins that are at least partially  
 CC encoded by the NHP sequences. Sequences derived from regions adjacent  
 CC to the intron/exon boundaries of NHP gene can be used to design primers  
 CC for use in amplification assays to detect mutations within the exons,  
 CC splice sites, introns that can be used in diagnostics and  
 CC pharmacogenomics. NHP sequences are utilized in microarrays or other  
 CC assay formats, to screen collections of genetic material from patients  
 CC who have a particular medical condition. NHP nucleotide sequences are  
 CC useful for drug screening effective in the treatment of symptomatic or  
 CC phenotypic manifestations of perturbing the normal function of NHP in the  
 CC body, and nucleotide constructs encoding NHP products are used to  
 CC genetically engineer host cells to express NHP products in vivo. These  
 CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
 CC protein to the body. Nucleotide constructs encoding NHP products are also  
 CC useful in gene therapy for modulating NHP expression. The encoded NHP  
 CC polypeptides are useful for generating antibodies, as reagents in  
 CC diagnostic assays, for identifying other cellular gene products related  
 CC to NHP and as reagents in assays for screening for compounds that are  
 CC useful in the treatment of mental, biological or medical disorders and  
 CC diseases. The gene for the NHPs is located on human chromosome 6.  
 XX The present sequence encodes an NHP of the invention.  
 SQ  
 Sequence 2688 BP; 540 A; 849 C; 871 G; 426 T; 2 other;  
 Query Match 15.0%; Score 37.8; DB 24; Length 2688;  
 Best Local Similarity 50.6%; Pred. No. 15;  
 Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
 QY 35 GTCCTGCGCGCTCCCACTCCCGAGGCGCCGAGAGGCGCCCGAGGAGCCCGAGTGCCTCG 94  
 Db 59 GCGCGTCCCGCGCGCGCTCCCGAGGAGATCGGGCGCGCGCGCGCGAGTGCCTCG 118  
 QY 95 ACGTTGCCACGCTGTGGATCAAGAGCGAGGAGCCAGAGGAGCCAGAACTGCGCGCGCGCG 154  
 Db 119 GTCGGAAGCGCGCGCGCGCGAGGAGGCGGATCAAGAGCGCGCGAGTGCCTCGCGCGCG 178



CC The present sequence encodes an NHP of the invention.  
XX Sequence 2856 BP; 529 A; 980 C; 897 G; 448 T; 2 other;  
SQ Query Match 15.0%; Score 37.8; DB 24; Length 2856;  
Best Local Similarity 50.6%; Pred. No. 15;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 35 GTCCTGAGCGCTCCACCTCCCGAGCGCAGAAAGCGCCCGACGAGGACCCCGAGTGCCTG 94  
DB 41 GCCGCTGCGCGCGCGCTGCGCCCAAGAGATCGGGGCGGGCGCGGAGATGATCCGG 100  
QY 95 ACGTTGCCACGCTGTGGGATCAGAGCGAGGACCGAGGACCGAGAACTGCGCGCGCCG 154  
DB 101 GTCGGAAGCGCGCGCGCGCGCGAGGAGCGGTACACCAACGCGCACTGAGCGCGCCG 160  
QY 155 GCCCTGCGCTGCGCGCGAGGAGAGCTCCCTCACGCGAGGAGAGCTCCCTCACCGCGG 212  
DB 161 GCCCGCGCGCGCGCGCGGGGATGCGCGCGCGCGAGCTGCTGCTCGCGCGCGCGCG 218  
RESULT 32  
ABX90553  
ID ABX90553 standard; cDNA; 2856 BP.  
AC ABX90553;  
XX 02-MAY-2003 (first entry)  
DE Human kinase cDNA #18.  
DE Human; gene; ss; kinase; phosphorylation; regulatory pathway;  
KM gene therapy.  
OS Homo sapiens.  
XX US2002161213-A1.  
FN 31-OCT-2002.  
PD 12-DEC-2001; 2001US-0020079.  
PF 12-DEC-2000; 2000US-255103P.  
PR 08-MAY-2001; 2001US-289422P.  
XX (TURN/) TURNER C A.  
PA (MATH/) MATHUR B.  
PA (FRID/) FRIDDLE C J.  
XX Turner CA, Mathur B, Friddle CJ;  
PI WPI; 2003-288125/28.  
DR P-PSDB; ABU60672.  
XX New novel human polynucleotides encoding proteins sharing sequence  
PT similarity with animal kinases, useful for diagnosing or creating  
PT disorders -  
XX Disclosure; Page 66-67; 78pp; English.  
PS The invention discloses isolated nucleic acids, and the protein that they  
CC encode, of novel human kinases. Kinases mediate the phosphorylation of a  
CC wide variety of proteins and compounds in the cell and are involved in a  
CC range of regulatory pathways. The novel human polynucleotides, encoding  
CC proteins sharing sequence similarity with animal kinases, are useful for  
CC diagnosing or treating (e.g. gene therapy) disorders. The sequence  
CC presented is a cDNA encoding a human kinase.  
XX Sequence 2856 BP; 529 A; 980 C; 897 G; 448 T; 2 other;  
SQ Query Match 15.0%; Score 37.8; DB 25; Length 2856;  
Best Local Similarity 50.6%; Pred. No. 15;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 35 GTCCTGAGCGCTCCACCTCCCGAGCGCAGAAAGCGCCCGACGAGGACCCCGAGTGCCTG 94  
DB 41 GCCGCTGCGCGCGCGCTGCGCCCAAGAGATCGGGGCGGGCGCGGAGATGATCCGG 100  
QY 95 ACGTTGCCACGCTGTGGGATCAGAGCGAGGACCGAGGACCGAGAACTGCGCGCGCCG 154  
DB 101 GTCGGAAGCGCGCGCGCGCGAGGAGCGGTACACCAACGCGCACTGAGCGCGCCG 160  
QY 155 GCCCTGCGCTGCGCGCGAGGAGAGCTCCCTCACGCGAGGAGAGCTCCCTCACCGCGG 212  
DB 161 GCCCGCGCGCGCGCGGGGATGCGCGCGCGCGAGCTGCTGCTCGCGCGCGCGCG 218  
RESULT 33  
ABK9890  
ID ABK9890 standard; cDNA; 2874 BP.  
AC ABK9890;  
XX 21-OCT-2002 (first entry)  
DE Human cDNA encoding a novel kinase protein #17.  
DE Human; ss; kinase; gene; nocotropic; gene therapy; novel human protein;  
KM NHP; serine-threonine kinase; casein kinase; mitogen activated kinase;  
KM calcium/calmodulin-dependent protein kinase; chromosome 6;  
KM mental disorder.  
OS Homo sapiens.  
XX WO200248333-A2.  
FN 20-JUN-2002.  
PD 12-DEC-2001; 2001WO-US49068.  
PF 12-DEC-2000; 2000US-255103P.  
PR 08-MAY-2001; 2001US-289422P.  
XX (LEXI-) LEXICON GENETICS INC.  
PA Turner CA, Mathur B, Friddle CJ;  
PI WPI; 2002-583505/62.  
DR P-PSDB; ABG69466.  
XX Novel polynucleotides encoding human proteins that are structurally  
PT related to animal kinases, useful for drug screening, diagnosis and in  
PT gene therapy of biological disorders -  
XX Disclosure; Page 82; 94pp; English.  
PS The invention relates to an isolated nucleic acid molecule comprising a  
CC nucleotide sequence encoding a novel human protein (NHP) appearing  
CC as ABG69450-ABG69469 that share structural similarity with animal  
CC kinases, including serine-threonine kinases, casein kinases, and  
CC calcium/calmodulin-dependent protein kinases, and mitogen activated  
CC kinases. NHP oligonucleotides are useful as hybridization probes for  
CC screening libraries and assessing gene expression patterns. NHP  
CC sequences are useful to identify mutations associated with a particular  
CC disease and also as a diagnostic or prognostic assay, and also in the  
CC molecular mutagenesis/evolution of proteins that are at least partially  
CC encoded by the NHP sequences. Sequences derived from regions adjacent  
CC to the intron/exon boundaries of NHP gene can be used to design primers  
CC for use in amplification assays to detect mutations within the exons,  
CC splice sites, introns that can be used in diagnostics and  
CC pharmacogenomics. NHP sequences are utilized in microarrays or other  
CC assay formats, to screen collections of genetic material from patients  
CC who have a particular medical condition. NHP nucleotide sequences are  
CC useful for drug screening effective in the treatment of symptomatic or  
CC phenotypic manifestations of perturbing the normal function of NHP in the  
CC body, and nucleotide constructs encoding NHP products are used to

CC genetically engineered host cells to express NHP products in vivo. These  
CC genetically engineered cells function as bioreactors in the body  
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
CC protein to the body. Nucleotide constructs encoding NHP products are also  
CC useful in gene therapy for modulating NHP expression. The encoded NHP  
CC polypeptides are useful for generating antibodies, as reagents in  
CC diagnostic assays, for identifying other cellular gene products related  
CC to NHP and as reagents in assays for screening for compounds that are  
CC useful in the treatment of mental, biological or medical disorders and  
CC diseases. The gene for the NHPs is located on human chromosome 6.  
CC The present sequence encodes an NHP of the invention.

SQ Sequence 2874 BP; 531 A; 983 C; 905 G; 453 T; 2 other;

Query Match 15.0%; Score 37.8; DB 24; Length 2874;

Best Local Similarity 50.6%; Pred. No. 15; Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 35 GTCCCTGCGCGCTCCGACCTCCGAGCGGAGAGCGCCCGACGAGACCCCGAGTCCCG 94  
DB 59 GCGCGTCCGCGCGCTCCGACCTCCGAGCGGAGCGGCGCGCGCGCGCGAGTATCCG 118  
QY 95 ACCTTGGCAGCGTCTGGATCAGAGCGAGGACCGAGACCGCAAGTCCCGCGCGCG 154  
DB 119 GTGCGAAGCGCGCGCGCGCGAGGAGCGGAGTCCCGACCGCGAGCTGAGCGCGCGCG 178  
QY 155 GCCCTGCGCGCGCGCGAGGAGTCCCTCAGCAGGAGGAGTCCCTCAGCGCGCG 212  
DB 179 GCCCGCGCGCGCGCGCGGAGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 236

RESULT 34  
ABK99887  
ID ABK99887 standard; cDNA; 2931 BP.

AC ABK99887;

DT 21-OCT-2002 (first entry)

DE Human cDNA encoding a novel kinase protein #14.

XX Human; ss; kinase; gene; noctropic; gene therapy; novel human protein;

KW NHP; serine-threonine kinase; casein kinase; mitogen activated kinase;

KM calcium/calmodulin-dependent protein kinase; chromosome 6;

XX mental disorder.

OS Homo sapiens.

PN WO200248333-A2.

PD 20-JUN-2002.

PF 12-DEC-2001; 2001WO-US49068.

PR 12-DEC-2000; 2000US-255103P.

PR 08-MAY-2001; 2001US-289422P.

PA (LEXI-) LEXICON GENETICS INC.

PI Turner CA, Machur B, Fridde CJ;

XX WPI, 2002-583505/62.

DR P-PSDB; ABG69463.

XX Novel polynucleotides encoding human proteins that are structurally

PT related to animal kinases, useful for drug screening, diagnosis and in

PS gene therapy of biological disorders

XX Disclosure; Page 72-73; 94pp; English.

XX The invention relates to an isolated nucleic acid molecule comprising a

CC nucleotide sequence encoding a novel human protein (NHP) appearing

CC as ABG69450-ABG69469, that share structural similarity with animal

CC kinases, including serine-threonine kinases, casein kinases,  
CC calcium/calmodulin-dependent protein kinases and mitogen activated  
CC kinases. NHP oligonucleotides are useful as hybridization probes for  
CC screening libraries and assessing gene expression patterns. NHP  
CC sequences are useful to identify mutations associated with a particular  
CC disease and also as a diagnostic or prognostic assay, and also in the  
CC molecular mutagenesis/evolution of proteins that are at least partially  
CC encoded by the NHP sequences. Sequences derived from regions adjacent  
CC to the intron/exon boundaries of NHP gene can be used to design primers  
CC for use in amplification assays to detect mutations within the exons,  
CC splice sites, introns that can be used in diagnostics and  
CC pharmacogenomics. NHP sequences are utilized in microarrays or other  
CC assay formats, to screen collections of genetic material from patients  
CC who have a particular medical condition. NHP nucleotide sequences are  
CC useful for drug screening effective in the treatment of symptomatic or  
CC phenotypic manifestations of perturbing the normal function of NHP in the  
CC body, and nucleotide constructs encoding NHP products are used to  
CC genetically engineer host cells to express NHP products in vivo. These  
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
CC protein to the body. Nucleotide constructs encoding NHP products are also  
CC useful in gene therapy for modulating NHP expression. The encoded NHP  
CC polypeptides are useful for generating antibodies, as reagents in  
CC diagnostic assays, for identifying other cellular gene products related  
CC to NHP and as reagents in assays for screening for compounds that are  
CC useful in the treatment of mental, biological or medical disorders and  
CC diseases. The gene for the NHPs is located on human chromosome 6.  
CC The present sequence encodes an NHP of the invention.

SQ Sequence 2931 BP; 569 A; 961 C; 915 G; 484 T; 2 other;

Query Match 15.0%; Score 37.8; DB 24; Length 2931;

Best Local Similarity 50.6%; Pred. No. 15; Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 35 GTCCCTGCGCGCTCCGACCTCCGAGCGGAGAGCGCCCGACGAGACCCCGAGTCCCG 94  
DB 41 GCGCGTCCGCGCGCGCGCGCGAGGAGTCCCGCGCGCGCGCGCGCGAGTATCCG 100  
QY 95 ACCTTGGCAGCGTCTGGATCAGAGCGAGGACCGAGACCGCAAGTCCCGCGCGCG 154  
DB 101 GTGCGAAGCGCGCGCGCGCGAGGAGCGGAGTCCCGACCGCGAGCTGAGCGCGCGCG 160  
QY 155 GCCCTGCGCGCGCGCGAGGAGTCCCTCAGCAGGAGGAGTCCCTCAGCGCGCG 212  
DB 161 GCCCGCGCGCGCGCGCGGAGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 218

RESULT 35  
ABX90549  
ID ABX90549 standard; cDNA; 2931 BP.

AC ABX90549;

DT 02-MAY-2003 (first entry)

DE Human kinase cDNA #14.

XX Human; gene; ss; kinase; phosphorylation; regulatory pathway;

KW gene therapy.

OS Homo sapiens.

PN US2002161213-A1.

PD 31-OCT-2002.

PF 12-DEC-2001; 2001US-0020079.

PR 12-DEC-2000; 2000US-255103P.

PR 08-MAY-2001; 2001US-289422P.

PA (TURN/) TURNER C A.

PA (MATH/) MATHUR B.  
 XX (FRID/) FRIDDLE C J.  
 XX PI Turner CA, Mathur B, Friddle CJ;  
 XX DR WPI: 2003-288125/28.  
 XX P-PSDB; AB060668.  
 PT New novel human polynucleotides encoding proteins sharing sequence  
 PT similarity with animal kinases, useful for diagnosing or treating  
 PT disorders -  
 XX Disclosure; Page 51-52; 78pp; English.  
 XX The invention discloses isolated nucleic acids, and the protein that they  
 CC encode, of novel human kinases. Kinases mediate the phosphorylation of a  
 CC wide variety of proteins and compounds in the cell and are involved in a  
 CC range of regulatory pathways. The novel human polynucleotides, encoding  
 CC proteins sharing sequence similarity with animal kinases, are useful for  
 CC diagnosing or treating (e.g. gene therapy) disorders. The sequence  
 CC presented is a cDNA encoding a human kinase.  
 XX  
 SQ Sequence 2931 BP; 569 A; 961 C; 915 G; 484 T; 2 other;  
 Query Match 15.0%; Score 37.8; DB 25; Length 2931;  
 Best Local Similarity 50.6%; Pred. No. 15;  
 Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
 OY 35 GTCCCTGAGCGCTCCACCTCCCGAGAGCGCGCCACGAGAACCCCACTGCTCCG 94  
 DB 41 GCCCGTGGCCCG 100  
 OY 95 ACCTTGCCACGCTGTGGATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 154  
 DB 101 GTCCGAGAGGCG 160  
 OY 155 GCCCCTGCGCTGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 212  
 DB 161 GCCCG 218

RESULT 36  
 ABK99886  
 ID ABK99886 standard; cDNA; 2949 BP.  
 XX  
 XX ABR99886;  
 DT 21-OCT-2002 (first entry)  
 XX  
 DE Human cDNA encoding a novel kinase protein #13.  
 XX  
 KW Human; ss; kinase; gene; neotropic; gene therapy; novel human protein;  
 KW NHP; serine-threonine kinase; casein kinase; mitogen activated kinase;  
 KW calcium/calmodulin-dependent protein kinase; chromosome 6;  
 KW mental disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200248333-A2.  
 XX  
 XX 20-JUN-2002.  
 XX  
 XX 12-DEC-2001; 2001WO-US49068.  
 XX  
 XX 12-DEC-2000; 2000US-255103P.  
 XX  
 XX 08-MAY-2001; 2001US-289422P.  
 XX  
 XX (LEXI-) LEXICON GENETICS INC.  
 XX  
 XX Turner CA, Mathur B, Friddle CJ;  
 XX  
 XX WPI: 2002-583505/62.  
 XX  
 XX P-PSDB; ABG69462.  
 XX

XX  
 PT Novel polynucleotides encoding human proteins that are structurally  
 PT related to animal kinases, useful for drug screening, diagnosis and in  
 PT gene therapy of biological disorders -  
 XX Disclosure; Page 69; 94pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid molecule comprising a  
 CC nucleotide sequence encoding a novel human protein (NHP) appearing  
 CC as ABG69450-ABG69469, that share structural similarity with animal  
 CC kinases, including serine-threonine kinases, casein kinases,  
 CC calcium/calmodulin-dependent protein kinases and mitogen activated  
 CC kinases. NHP oligonucleotides are useful as hybridisation probes for  
 CC screening libraries and assessing gene expression patterns. NHP  
 CC sequences are useful to identify mutations associated with a particular  
 CC disease and also as a diagnostic or prognostic assay, and also in the  
 CC molecular mutagenesis/evolution of proteins that are at least partially  
 CC encoded by the NHP sequences. Sequences derived from regions adjacent  
 CC to the intron/exon boundaries of NHP gene can be used to design primers  
 CC for use in amplification assays to detect mutations within the exons,  
 CC splice sites, introns that can be used in diagnostics and  
 CC pharmacogenomics. NHP sequences are utilised in microarrays or other  
 CC assay formats, to screen collections of genetic material from patients  
 CC who have a particular medical condition. NHP nucleotide sequences are  
 CC useful for drug screening effective in the treatment of symptomatic or  
 CC phenotypic manifestations of perturbing the normal function of NHP in the  
 CC body, and nucleotide constructs encoding NHP products are used to  
 CC genetically engineer host cells to express NHP products in vivo. These  
 CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
 CC protein to the body. Nucleotide constructs encoding NHP products are also  
 CC useful in gene therapy for modulating NHP expression. The encoded NHP  
 CC polypeptides are useful for generating antibodies, as reagents in  
 CC diagnostic assays, for identifying other cellular gene products related  
 CC to NHP and as reagents in assays for screening for compounds that are  
 CC useful in the treatment of mental, biological or medical disorders and  
 CC diseases. The gene for the NHPs is located on human chromosome 6.  
 CC The present sequence encodes an NHP or the invention.  
 XX  
 SQ Sequence 2949 BP; 571 A; 964 C; 923 G; 489 T; 2 other;  
 Query Match 15.0%; Score 37.8; DB 24; Length 2949;  
 Best Local Similarity 50.6%; Pred. No. 15;  
 Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
 OY 35 GTCCCTGAGCGCTCCACCTCCCGAGAGCGCGCCACGAGAACCCCACTGCTCCG 94  
 DB 59 GCCCGTGGCCCG 118  
 OY 95 ACCTTGCCACGCTGTGGATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 154  
 DB 119 GTCCGAGAGGCG 178  
 OY 155 GCCCCTGCGCTGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 212  
 DB 179 GCCCG 236

RESULT 37  
 ABK90548  
 ID ABK90548 standard; cDNA; 2949 BP.  
 XX  
 XX ABX90548;  
 DT 02-MAY-2003 (first entry)  
 XX  
 DE Human kinase cDNA #13.  
 XX  
 KW Human; gene; ss; kinase; phosphorylation; regulatory pathway;  
 KW gene therapy.  
 XX  
 XX Homo sapiens.  
 XX

PN US2002161213-A1.  
XX  
XX 31-OCT-2002.  
XX  
PF 12-DEC-2001; 2001US-0020079.  
XX  
PR 12-DEC-2000; 2000US-255103P.  
XX 08-MAY-2001; 2001US-289422P.  
XX  
XX (TURN/) TURNER C A.  
XX (MATH/) MATHUR B.  
XX (FRID/) FRIDDLE C J.  
XX  
XX Turner CA, Mathur B, Friddle CJ;  
XX WPI; 2003-288125/28.  
XX P-PSDB; ABUS0667.  
XX  
XX New novel human polynucleotides encoding proteins sharing sequence  
XX similarity with animal kinases, useful for diagnosing or treating  
XX disorders -  
XX  
XX Disclosure; Page 47-48; 78pp; English.  
XX  
XX The invention discloses isolated nucleic acids, and the protein that they  
XX encode, of novel human kinases. Kinases mediate the phosphorylation of a  
XX wide variety of proteins and compounds in the cell and are involved in a  
XX range of regulatory pathways. The novel human polynucleotides, encoding  
XX proteins sharing sequence similarity with animal kinases, are useful for  
XX diagnosing or treating (e.g. gene therapy) disorders. The sequence  
XX presented is a cDNA encoding a human kinase.  
XX  
SQ Sequence 2949 BP; 571 A; 964 C; 923 G; 489 T; 2 other;  
Query Match 15.0%; Score 37.8; DB 25; Length 2949;  
Best Local Similarity 50.6%; Pred. No. 15;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
OY 35 GTCCCTGCGGCTCCACCTCCCAAGGCGCAGAGAGCCGCCAGAGACCCCGATGCCCC 94  
DB 59 GCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 118  
OY 95 ACGTTGCCAGGATCGGATCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 154  
DB 119 GTGGAGAGCGCGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 178  
OY 155 GCCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 212  
DB 179 GCCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 236  
RESULT 38  
AAV94191/C  
ID AAV94191 standard; DNA; 5418 BP.  
AC AAV94191;  
XX  
XX 22-MAY-1998 (first entry)  
XX  
XX Promoter region of pig complement inhibitor DNA.  
XX  
XX Promoter region; pig complement inhibitor DNA; thrombomodulin;  
XX transgenic pig; hyperacute rejection; organ transplant;  
XX tissue transplant; ds.  
XX  
XX Sus scrofa.  
XX  
XX Key Location/Qualifiers  
XX misc\_feature 3797..5418  
XX FT /tag= a  
XX FT /note= "Preferred 1.7 kb fragment of claim 3"  
XX  
XX WO9744449-A1.

XX  
XX 27-NOV-1997.  
XX  
XX 19-MAY-1997; 97MO-JP01677.  
XX  
XX 17-MAY-1996; 96JP-0148335.  
XX  
XX (NIME-) NIPPON MEAT PACKERS INC.  
XX  
XX Fujimura T, Murakami H, Shigenisa T, Toyomura K;  
XX WPI; 1998-018504/02.  
XX  
XX Pig complement inhibitor promoter sequence - allows human complement  
XX inhibitor to be expressed efficiently in transgenic pigs  
XX  
XX Claim 1; Pages 13-16; 27pp; Japanese.  
XX  
XX The present sequence is the promoter region of pig complement  
XX inhibitor DNA. It allows human complement inhibitors or other  
XX thrombus formation inhibiting factors (e.g. thrombomodulin) to be  
XX expressed efficiently in transgenic pigs, when inserted upstream of  
XX a human DNA sequence. This prevents hyperacute rejection when  
XX organs or tissue from the transgenic pigs are transplanted into  
XX humans.  
XX  
SQ Sequence 5418 BP; 1578 A; 1261 C; 1109 G; 1409 T; 61 other;  
Query Match 15.0%; Score 37.8; DB 19; Length 5418;  
Best Local Similarity 53.8%; Pred. No. 15;  
Matches 78; Conservative 0; Mismatches 67; Indels 0; Gaps 0;  
OY 38 CCTGCGGCTCCACCTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 97  
DB 5298 CGTGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5239  
OY 98 TTGCCACGGTCTGGATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 157  
DB 5238 GAGCCAAATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 5179  
OY 158 CCTGCCCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 182  
DB 5178 GAGAGAGGAGCGCCCTTGTCTCTCC 5154  
RESULT 39  
AAV73802  
ID AAV73802 standard; DNA; 35100 BP.  
XX  
XX AAV73802;  
XX  
XX 25-FEB-1999 (first entry)  
XX  
XX KSHV LTR DNA (nucleotides 1-35,100).  
XX  
XX  
XX Kapoli's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2;  
XX dihydrofolate reductase; LTR; long unique region; vaccine; Propylaxia;  
XX diagnosis; treatment; BHV8; complement binding protein; V-CB; SSBP;  
XX ssDNA binding protein; transport protein; glycoprotein B; pol; VIL-6;  
XX DNA polymerase; viral interleukin-6; BHV4-IE1 I; thymidylate synthase;  
XX VMLP-11; BHV4-IE1 II; VMLP-I; capsid protein I; tegument protein I; ds.  
XX  
XX Kapoli's sarcoma-associated herpesvirus.  
XX  
XX US5849564-A.  
XX  
XX 15-DEC-1998.  
XX  
XX 29-NOV-1996; 96US-0770379.  
XX  
XX 29-NOV-1996; 96US-0770379.  
XX  
XX (UYCO ) UNIV COLUMBIA NEW YORK.



PS Example 2; Page 135-203; 230pp; English.

XX  
CC This sequence represents the long unique region and terminal repeat of  
CC the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known  
CC as human herpes virus 8 (HHV8). This sequence contains the DNAs of the  
CC invention which encode KSHV polypeptides selected from: (a) viral  
CC macrophage inflammatory protein (MIP) II; (b) viral interleukin-6 (IL-6);  
CC (c) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L;  
CC (d) capsid protein IV encoded by ORF65; and (e) immediate early protein  
CC encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded  
CC by it, and antibodies (Ab) specific for the proteins are useful for  
CC detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body  
CC fluids or tissue samples. HHV8 infections can be treated with antisense  
CC or triplex forming molecules or agents that bind specifically to the  
CC protein. Ab may be used for prophylaxis or treatment of HHV8 infection,  
CC while the protein can be used in protective vaccines. Ab may also be used  
CC to differentiate between lymphomas, and HHV8 may be implicated in many  
CC other lymphoproliferative diseases such as lymphomas, leukaemia,  
CC splenomegaly and mycosis fungoides. Cells and animals containing the  
CC nucleic acid are useful for drug screening. HHV8-derived peptides can be  
CC used as targets for antiviral drugs, e.g. dihydrofolate reductase gene  
CC can be inhibited with methotrexate. These can also be used to determine  
CC the immune status of a patient infected with HIV. HHV8 derived protein  
CC viral MIP II may be used as an anti-inflammatory agent for,  
CC e.g. treating rheumatoid arthritis. This sequence is stated as containing  
XX 81 open reading frames!

SQ Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;

Query Match 15.0%; Score 37.8; DB 19; Length 137507;

Best Local Similarity 50.0%; Pred. No. 15; Indels 4; Gaps 1;

Matches 122; Conservative 0; Mismatches 118; Indels 4; Gaps 1;

QY	2	GGCCGGGAGGCGCGGAGTGAGGCTGATGTCCTGCGCCTCCACTCCCGAGGC	61
DB	24529	GGCCCGGAGGCGCGGAGTGAGGCTGATGTCCTGCGCCTCCACTCCCGAGGC	24588
QY	62	GCAGAAGGCGCCACGAGAGCCCGCAGTGCCTCCAGCTTGCCAGGCTCGGATCAGAGGC	121
DB	24589	GGCCCGGAGGCGCGGAGTGAGGCTGATGTCCTGCGCCTCCACTCCCGAGGC	24648
QY	122	---AGGAGCCAGGAGGAGCACTGCGCCCGCCCGCCCTGCGCCTGCGCGAGGGA	177
DB	24649	GGCACCCTCCCGGAGGAGGATCCCGGCGCCGACCTCCCGAGGAGGATCCCGGCGC	24708
QY	178	GCTCCCTACGAGGAGAGTCCCTCTACCCGCGCCAGCCCTGCAAGGAGGCGCGTGGG	237
DB	24709	GGCACCCTCCCGGAGGAGGATCCCGGCGCCGACCTCCCGGAGGAGGATCCCGGCGC	24768
QY	238	GTCA	241
DB	24769	GCCA	24772

Search completed: November 6, 2003, 07:07:34  
Job time : 184.882 secs





```
RESULT 2
US-09-471-867-1
; Sequence 1, Application US/09471867
; Patent No. 6455289
; GENERAL INFORMATION:
; APPLICANT: Uchimura, Kenji
; APPLICANT: Muramatsu, Hideki
; APPLICANT: Kadomatsu, Kenji
; APPLICANT: Kannagi, Reiji
; APPLICANT: Habuchi, Osamu
; APPLICANT: Muramatsu, Takashi
; TITLE OF INVENTION: POLYPEPTIDE OF N-ACETYLGLUCOSAMINE-6-0-SULFOTRANSFERASE AND
; FILE REFERENCE: TOYAMA1.001AUS
; CURRENT APPLICATION NUMBER: US/09/471,867
; EARLIER FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: US 09/263,023
; EARLIER FILING DATE: 1999-03-05
; EARLIER APPLICATION NUMBER: JP 10-54007
; EARLIER FILING DATE: 1998-03-05
; EARLIER APPLICATION NUMBER: JP 10-177844
; EARLIER FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (470) .. (1918)
US-09-471-867-1
Query Match 16.7%; Score 42.2; DB 4; Length 2150;
Best Local Similarity 50.0%; Pred. No. 0.17;
Matches 104; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 28 CCGATGCTGCTGCGGCGCTCCACCTCCCGGCGAGAGGCGCGCCAGAGACCCCA 87
DB 143 CAGAGCTCTTCTGCGAGCGCGCTGATGAGGAGCGAGCGCGCGCGGAGACCA 202
QY 88 GAGCGCGAGCTTCCAGCGCTGAGATCAGAGGAGGAGCGAGGAGCGAGAACTGGGC 147
DB 203 GCGCTGCGCGCGCGCGCGCGCGCTCGATCGGCGCGCGCGCGCGCGCGCGAGC 262
QY 148 CGCGCGCGCGCGCTGCGCTGCGCGCGCGAGGAGGAGCTCCCTCAGAGGAACTCCCTCAG 207
DB 263 TCGAGGCTCCCTCTCTGAGGCTGCGAGGCGCGCGCTCCGCGCGCGCGCGCGCTGTG 322
QY 208 CGGCGCGAGCGCTGCGAGGCGCGCGCGCTG 235
DB 323 CCTGTGATGAGCGCGAGCTCGCGCGAG 350
RESULT 3
US-09-376-728-1/c
; Sequence 1, Application US/09376728
; Patent No. 6372961
; GENERAL INFORMATION:
; APPLICANT: Tarczyński, Mitchell C.
; APPLICANT: Shen, Bo
; TITLE OF INVENTION: Hemoglobin Genes and Their Use
; FILE REFERENCE: 0873
; CURRENT APPLICATION NUMBER: US/09/376,728
; EARLIER FILING DATE: 1999-08-17
; EARLIER APPLICATION NUMBER: US 60/097,242
; EARLIER FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 840
```

```
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (51) ... (623)
US-09-376-728-1
Query Match 15.3%; Score 38.6; DB 4; Length 840;
Best Local Similarity 52.5%; Pred. No. 1.1;
Matches 83; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 51 CCTCCCGAGCGAGAGGCGCCAGAGAGCCCGAGTCCCGAGCTTGCCAGCGTCTG 110
DB 465 CCTCTCCAGCGCGCGCTTCATCTCCGCGGTCCAGATGTCGGGACCGGTCTGATG 406
QY 111 GATCAGAGGCGAGGAGCCAGAGGAGCGAGAACTGGCGCGCGCGCGCGCTGCGGCG 170
DB 405 TGTCCAGCAGCGCGCGCTTTGACACCTCGAAATGCCGCTGCGAGCGCGCGCTGCGT 346
QY 171 GAGGAACTCCCTCAGCAGAGGAGGAGCTCCCTCAGC 208
DB 345 GCGTCGCGCGCGAGCGCGCTTCAAGGATGAGCTCTCCCTCAGC 308
RESULT 4
US-09-679-279-25/c
; Sequence 25, Application US/09679279
; Patent No. 6524841
; GENERAL INFORMATION:
; APPLICANT: McDaniel, Robert
; APPLICANT: Volchegursky, Yanina
; TITLE OF INVENTION: Recombinant Megalomicin Biosynthetic
; FILE REFERENCE: 300622004700
; CURRENT APPLICATION NUMBER: US/09/679,279
; CURRENT FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/158,305
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 60/190,024
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Micromonospora megalomicae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (528)
; OTHER INFORMATION: Sequence with codon changes as described in the
; Patent No. 6524841
; OTHER INFORMATION: specification at page 99, line 22 thru page 101, line 23
US-09-679-279-25
Query Match 15.2%; Score 38.2; DB 4; Length 528;
Best Local Similarity 48.2%; Pred. No. 1.3;
Matches 106; Conservative 0; Mismatches 114; Indels 0; Gaps 0;
QY 14 GGGCGGAGTGAAGCTGATCTGCTGCGCGCTCCAGCTCCCGAGGCGCGAGAGCGCC 73
DB 300 GGGCTTGACGCTGCGCAGACAGCGAGCGCGCGCGCGCGCGCGCGCGCTTACGTGC 241
QY 74 CACGAGAGCCCGAGGCGCGAGCTGCGAGCTGAGATCAGAGGCGAGGAGCGAGGAG 133
DB 240 CAGAGAGGCGCGCGAGCTGAGCGAGATCCCGAGGCGGCGGTCGAGTGGCGCTCGAC 181
QY 134 GCGAGAGCTGCGCGCGCGCGCGCGCGCTGCGCGCGCGAGGAGAACTCCCTCAGCGAG 193
DB 180 GACTCGAGCTGCGCGCGCGCGCGCGCGATCTCGCGCGCTCCCGAGCGCGCGATACCGCTG 121
QY 194 GAGCTTCCTCAGCGCGCGCGCGCGCGCTGAGAGGCGCGCG 233
DB 120 CTGGCGAGACCGAGAGGCGCGCGCGCGCGCGCTTTAGCGG 81
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```
RESULT 5
US-09-039-609-1
; Sequence 1, Application US/09039609
; Patent No. 6107473
; GENERAL INFORMATION:
; APPLICANT: ALBONE, EARL
; APPLICANT: KIKLY, KRISTINE
; TITLE OF INVENTION: A KRINGLE-RELATED CLONE,
; TITLE OF INVENTION: HTHE247
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,609
; FILING DATE: 16-MAR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/060,623
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70275
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1875 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-039-609-1

Query Match          15.1%; Score 38; DB 3; Length 1875;
Best Local Similarity 49.2%; Pred. No. 1.5;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 52 CTCGCCAGGCGCAGAGAGCGCCCAAGAGAGACCCCAAGTGCCTGACGTTGCGACGCTCTGG 111
Db 1 CTCGCCCTGTCTCCCATGTGCGCGCCCGCCGCTCTCCCGCTTACCCCGGGCGCG 60

QY 112 GATCAGAGGAGGAGGAGCCAGGAGAGCTGCGCGCCCGCCCGCCCTGCTGCGCG 171
Db 61 GCCCGCGGGGCGCCGCACTGACGCGCCCATGCGCGCCGAGCGCCCGCCCTGCTGCT 120

QY 172 AGGGAAGCTCCTCCTACGCGAGGAGAGTCCCTCCTACCGCGCGCCCTGCTGCGCG 231
Db 121 CCGCGCGGCGGCTCAGCGTGGCGCGCCCGCGCGCTTACCGCGCGCTGCGCGCGGAC 180

QY 232 CGTGGGCTCAGACCGGAAA 250
Db 181 CCGAGTGTTCACAGCCAA 199

RESULT 6
US-09-180-939-2/C
; Sequence 2, Application US/09180939A
; Patent No. 6255474
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```
; GENERAL INFORMATION:
; APPLICANT: TOTOMURA, KOJI
; APPLICANT: FUJIMURA, Tatsuya
; APPLICANT: MORAKAMI, Hiroshi
; APPLICANT: SHIGEMISA, Tamotsu
; TITLE OF INVENTION: A Promoter Gene for a Porcine Complement Inhibitor
; FILE REFERENCE: 2520-0116P
; CURRENT APPLICATION NUMBER: US/09/180,939A
; EARLIER FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: PCT/JP97/01677
; EARLIER FILING DATE: 1997-05-19
; EARLIER APPLICATION NUMBER: 148335/1996 JAPAN
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1622
; TYPE: DNA
; ORGANISM: Porcine sp.
; US-09-180-939-2

Query Match          15.0%; Score 37.8; DB 3; Length 1622;
Best Local Similarity 53.8%; Pred. No. 1.6;
Matches 78; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 38 CTTGGCGCTTCACTCCCAAGCGCGCAGAGCGCCCAAGAGACCCCAAGTGCCTGCGAGC 97
Db 1502 CGTGGCTGTGGGCGCCGCTGTGGAGAGTGTCTTGAAGAGTGACTCCAGAGGCGCGCG 1443

QY 98 TTGCCACGGTCTGGAGATCAGAGGAGGAGCCAGGAGCCAGGAGACTGCGCCCGCCCGCG 157
Db 1442 GAGCCATATGGGCGGCGCGGCGGAGCGGCGCTGTGGGCGCGGCGCGGCGGCGCTCGGCG 1383

QY 158 CCTGCCCTTGGCGCGCAGGAGAGCTCC 182
Db 1382 GAGAGAGGAGCGCCCTTGTCTCC 1358

RESULT 7
US-10-020-079-11
; Sequence 11, Application US/10020079
; Patent No. 6579710
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fridlie, Carl Johan
; TITLE OF INVENTION: No. 6579710e1 Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-020-079-11

Query Match          15.0%; Score 37.8; DB 4; Length 1947;
Best Local Similarity 50.6%; Pred. No. 1.6;
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 35 GTCCCTGGGCGCTTCACTCCCAAGCGCGCAGAGCGCCCAAGAGACCCCAAGTGCCTGCG 94
Db 41 GCCGCTGCCCGCGCCCTCTGCCCAAGAGAGATCGGGCGCGCGCGCGCGCGAGATATCCGG 100

QY 95 ACCTTGCCACGGTCTGGAGATCAGAGGAGGAGACCAAGAGCCAGAGAACTGCGCGCGCGCG 154
Db 101 GTCCGAGAGCGCGCGCGCGCGAGAGGAGGAGTCAACCGCCCGCACTGAGCGCGCGCGCG 160
```

QY 155 GCCCCTGCGCTGGGCGGAGGAGTCCCTCAACGAGGAGAACTCCCTCAACCCGGC 212  
Db 161 GCCCGCGCGCGCGCGCGGAGATGCGCGCCCGCAAGCTCTGCTCCGCGCGCGCGC 218

## RESULT 8

US-10-020-079-9  
; Sequence 9, Application US/10020079  
; Patent No. 6579710  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6579710e1 Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1965  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-9

Query Match 15.0%; Score 37.8; DB 4; Length 1965;  
Best Local Similarity 50.6%; Pred. No. 1.6;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 35 GTCCCTGCGCTGGGCGGAGGAGTCCCTCAACGAGGAGAACTCCCTCAACCCGGC 94  
Db 59 GCCGCTGCGCGCGCGCGGAGATGCGCGCCCGGCGCGGAGATGATCCGG 118  
QY 95 ACCTTCCACGAGTCTGAGATCAGAGGACGAGGACCAAGGAGCCAGAACTGCGCGCGCC 154  
Db 119 GTCGAAGGCGCGCGCGCGCGGAGGAGCGGATCACCACCGCGCATGAGCGCGCC 178  
QY 155 GCCCCTGCGCTGGGCGGAGGAGTCCCTCAACGAGGAGAACTCCCTCAACCCGGC 212  
Db 179 GCCCGCGCGCGCGCGGAGATGCGCGCCCGCAAGCTGCTGCTCCGCGCGCGCGC 236

## RESULT 9

US-10-020-079-3  
; Sequence 3, Application US/10020079  
; Patent No. 6579710  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6579710e1 Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 2595  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-3

Query Match 15.0%; Score 37.8; DB 4; Length 2595;  
Best Local Similarity 50.6%; Pred. No. 1.7;

Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 35 GTCCCTGCGCTGGGCGGAGGAGTCCCTCAACGAGGAGAACTCCCTCAACCCGGC 94  
Db 41 GCCGCTGCGCGCGCGCGGAGATGCGCGCCCGCAAGGATGCGGCGCGCGGAGATGCGG 100  
QY 95 ACCTTCCACGAGTCTGAGATCAGAGGACGAGGACCAAGGAGCCAGAACTGCGCGCGCC 154  
Db 101 GTCGAAGGCGCGCGCGCGGAGGAGGATGCGCGCCCGCAAGGATGCGGCGCGCGCGC 160  
QY 155 GCCCCTGCGCTGGGCGGAGGAGTCCCTCAACGAGGAGAACTCCCTCAACCCGGC 212  
Db 161 GCCCGCGCGCGCGCGGAGATGCGCGCCCGCAAGCTGCTGCTCCGCGCGCGCGC 218

## RESULT 10

US-10-020-079-1  
; Sequence 1, Application US/10020079  
; Patent No. 6579710  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6579710e1 Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2613  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-1

Query Match 15.0%; Score 37.8; DB 4; Length 2613;  
Best Local Similarity 50.6%; Pred. No. 1.7;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 35 GTCCCTGCGCTGGGCGGAGGAGTCCCTCAACGAGGAGAACTCCCTCAACCCGGC 94  
Db 59 GCCGCTGCGCGCGCGCGGAGATGCGCGCCCGGCGCGGAGATGATCCGG 118  
QY 95 ACCTTCCACGAGTCTGAGATCAGAGGACGAGGACCAAGGAGCCAGAACTGCGCGCGCC 154  
Db 119 GTCGAAGGCGCGCGCGCGGAGGAGCGGATCACCACCGCGCATGAGCGCGCC 178  
QY 155 GCCCCTGCGCTGGGCGGAGGAGTCCCTCAACGAGGAGAACTCCCTCAACCCGGC 212  
Db 179 GCCCGCGCGCGCGCGGAGATGCGCGCCCGCAAGCTGCTGCTCCGCGCGCGCGC 236

## RESULT 11

US-10-020-079-19  
; Sequence 19, Application US/10020079  
; Patent No. 6579710  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6579710e1 Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 2670  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-19

Query Match  
Best Local Similarity 15.0%; Score 37.8; DB 4; Length 2670;  
Matches 90; Conservativity 0; Mismatches 88; Indels 0; Gaps 0;

QY 35 GTCCCTGGGCGCTCCACCTCCCGACGAGAGGCGCCCGACGAGACCCCGAGTCCCG 94  
DB 41 GCCGCTGCGCGCGCGCTCCCGACGAGAGGCGCGGTCACCCAGCCCGACGAGCCCGCC 100  
QY 95 ACCTTGCACAGTCTGGATCAGAGGACGAGGACCGAGGACCGAGAACTGCGCGCGCC 154  
DB 101 GTCGAAGGCGCGCGCGCGCGGAGGAGCGGTCACCCAGCCCGACGAGCCCGCC 160  
QY 155 GCCCTGCGCGCTCCGCGGAGGAGGAGTCCCTCACGAGGAGGAGTCCCTCACCGCG 212  
DB 161 GCCCGCGCGCGCGCGCGGAGGAGGCGCGCGCTGCTGCTCGCGCGCGCGCG 218

RESULT 12  
US-10-020-079-17  
; Sequence 17, Application us/10020079  
; Patent No. 6579710  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Fridde, Carl Johan  
; TITLE OF INVENTION: No. 6579710el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 2688  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-17

Query Match  
Best Local Similarity 15.0%; Score 37.8; DB 4; Length 2688;  
Matches 90; Conservativity 0; Mismatches 88; Indels 0; Gaps 0;

QY 35 GTCCCTGGGCGCTCCACCTCCCGACGAGAGGCGCCCGACGAGACCCCGAGTCCCG 94  
DB 59 GCCGCTGCGCGCGCGCTCCCGACGAGAGGCGCGGTCACCCAGCCCGACGAGCCCGCC 118  
QY 95 ACCTTGCACAGTCTGGATCAGAGGACGAGGACCGAGGACCGAGAACTGCGCGCGCC 154  
DB 119 GTCGAAGGCGCGCGCGCGGAGGAGGAGTCCCTCACGAGGAGGAGTCCCTCACCGCG 178  
QY 155 GCCCTGCGCGCTCCGCGGAGGAGGAGTCCCTCACGAGGAGGAGTCCCTCACCGCG 212  
DB 179 GCCCGCGCGCGCGCGCGGAGGAGGCGCGCGCTGCTGCTCGCGCGCGCGCG 236

RESULT 13  
US-10-020-079-35  
; Sequence 35, Application us/10020079  
; Patent No. 6579710  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Fridde, Carl Johan  
US-10-020-079-35

FILE OF INVENTION: No. 6579710el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: us/10/020,079  
; CURRENT FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 2856  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-35

Query Match  
Best Local Similarity 15.0%; Score 37.8; DB 4; Length 2856;  
Matches 90; Conservativity 0; Mismatches 88; Indels 0; Gaps 0;

QY 35 GTCCCTGGGCGCTCCACCTCCCGACGAGAGGCGCCCGACGAGACCCCGAGTCCCG 94  
DB 41 GCCGCTGCGCGCGCGCTCCCGACGAGAGGCGCGGTCACCCAGCCCGACGAGCCCGCC 100  
QY 95 ACCTTGCACAGTCTGGATCAGAGGACGAGGACCGAGGACCGAGAACTGCGCGCGCC 154  
DB 101 GTCGAAGGCGCGCGCGCGCGGAGGAGCGGTCACCCAGCCCGACGAGCCCGCC 160  
QY 155 GCCCTGCGCGCTCCGCGGAGGAGGAGTCCCTCACGAGGAGGAGTCCCTCACCGCG 212  
DB 161 GCCCGCGCGCGCGCGCGGAGGAGGCGCGCGCTGCTGCTCGCGCGCGCGCGCG 218

RESULT 14  
US-10-020-079-33  
; Sequence 33, Application us/10020079  
; Patent No. 6579710  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Fridde, Carl Johan  
; TITLE OF INVENTION: No. 6579710el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 2874  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-33

Query Match  
Best Local Similarity 15.0%; Score 37.8; DB 4; Length 2874;  
Matches 90; Conservativity 0; Mismatches 88; Indels 0; Gaps 0;

QY 35 GTCCCTGGGCGCTCCACCTCCCGACGAGAGGCGCCCGACGAGACCCCGAGTCCCG 94  
DB 59 GCCGCTGCGCGCGCGCTCCCGACGAGAGGCGCGGTCACCCAGCCCGACGAGCCCGCC 118  
QY 95 ACCTTGCACAGTCTGGATCAGAGGACGAGGACCGAGGACCGAGAACTGCGCGCGCC 154  
DB 119 GTCGAAGGCGCGCGCGCGGAGGAGGAGTCCCTCACGAGGAGGAGTCCCTCACCGCG 178  
QY 155 GCCCTGCGCGCTCCGCGGAGGAGGAGTCCCTCACGAGGAGGAGTCCCTCACCGCG 212  
DB 179 GCCCGCGCGCGCGCGCGGAGGAGGCGCGCGCTGCTGCTCGCGCGCGCGCGCG 236

RESULT 15  
US-10-020-079-27  
; Sequence 27, Application US/10020079  
; Patent No. 6579710  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Fiddler, Carl Johan  
; TITLE OF INVENTION: No. 6579710el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0281,USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 2931  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-27

Query Match 15.0%; Score 37.8; DB 4; Length 2931;  
Best Local Similarity 50.6%; Pred. No. 1.7;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 35 GTCCTGCGCCCTCTCACTTCCAGGCGCAAGAGCGCCCGCCAGAGAGCCCGCCAGTCCCG 94  
DB 41 GCCGTCGCGCCCGCCCTGTCGCAAGAGAGATCGGGCCGGCCGGCGGATGATCCGG 100  
QY 95 ACCTTCCACGATCTGTGGATCAGAGCAGAGGAGCCAGAGAGCCAGAACTGCGCCGCC 154  
DB 101 GTGCGAAGCGCGCGCGCGCGCGAGAGCGGGTCAACCACCGCCGACAGAGCGCGCC 160

QY 155 GCCCTGCGCCCTCTCACTTCCAGGCGCAAGAGCGCCCGCCAGAGAGCCCGCCAGTCCCG 212  
DB 161 GCCCGCGCGCGCGCGCGCGCGAGATGCGCCCGCCGAGAGCTGTGCTCGCGCGCGCG 218

RESULT 16  
US-10-020-079-25  
; Sequence 25, Application US/10020079  
; Patent No. 6579710  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Fiddler, Carl Johan  
; TITLE OF INVENTION: No. 6579710el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0281,USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 2949  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-25

Query Match 15.0%; Score 37.8; DB 4; Length 2949;  
Best Local Similarity 50.6%; Pred. No. 1.7;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 35 GTCCTGCGCCCTCTCACTTCCAGGCGCAAGAGCGCCCGCCAGAGAGCCCGCCAGTCCCG 94  
DB 59 GCCCTGCGCGCCCGCCCTGTCGCAAGAGAGATCGGGCGCGCGCGCGCGAGTATCCGG 118

QY 95 ACCTTCCACGATCTGTGGATCAGAGCGAGGAGCCAGAGAGCCCGCCAGTCCCGCCCG 154  
DB 119 GTGCGAAGCGCGCGCGCGCGCGAGAGCGGGTCAACCACGCGGACGTAGCGCGCC 178

QY 155 GCCCTGCGCCCTCTGAGCGCGAGAGAGCTTCTACACGAGAGAGAGCTTCTACCGCG 212  
DB 179 GCCCGCGCGCGCGCGCGCGAGATGCGCGCGCCCGCCAGAGCTGTGCTCGCGCGCGCG 236

RESULT 17  
US-09-180-939-1/c  
; Sequence 1, Application US/09180939A  
; Patent No. 625474  
; GENERAL INFORMATION:  
; APPLICANT: TOYOMURA, Koji  
; APPLICANT: FUJIMURA, Tatsuya  
; APPLICANT: MURAKAMI, Hiroshi  
; APPLICANT: SHIGEMISHI, Tamotsu  
; TITLE OF INVENTION: A Promoter Gene for a Porcine Complement Inhibitor  
; FILE REFERENCE: 2520-0116P  
; CURRENT APPLICATION NUMBER: US/09/180,939A  
; PRIOR FILING DATE: 1998-11-17  
; EARLIER APPLICATION NUMBER: PCT/JP97/01677  
; EARLIER FILING DATE: 1997-05-18  
; EARLIER APPLICATION NUMBER: 148335/1996 JAPAN  
; EARLIER FILING DATE: 1996-05-17  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 5418  
; TYPE: DNA  
; ORGANISM: Porcine sp.  
; FEATURE:  
; OTHER INFORMATION: n = G, C, A, or T  
US-09-180-939-1

Query Match 15.0%; Score 37.8; DB 3; Length 5418;  
Best Local Similarity 53.8%; Pred. No. 1.7;  
Matches 78; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 38 CCTGCGCCCTCTCACTTCCAGGCGCAAGAGCGCCCGCCAGAGAGCCCGCCAGTCCCG 97  
DB 5298 CGTGCGCTGAGCGCCCGCGCTGCGCGAGAGTGGCTTAAGGAGTGAATCCAGGCGCGCG 5239

QY 98 TTGCGACGATCTGTGGATCAGAGCGAGGAGCCAGAGAGCCAGAACTGCGCGCGCGCG 157  
DB 5238 GAGCCATATGAGCGCGCGCGCGCGAGCGCGCGCTGTGGGCGGGCGGGGCGGCGCTCGCG 5179

QY 158 CCTGCGCCCTCTGAGCGAGAGAGAGTCC 182  
DB 5178 GAGAGAGAGAGCGCTTGTGCTTC 5154

RESULT 18  
US-08-770-379-17  
; Sequence 17, Application US/08770379  
; Patent No. 5849564  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Yuan  
; APPLICANT: Bohenzky, Roy A.  
; APPLICANT: Russo, James J.  
; APPLICANT: Edelman, Isidore S.  
; APPLICANT: Moore, Patrick S.  
; TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.

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; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,379
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 52342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-770-379-17

Query Match          15.0%; Score 37.8; DB 2; Length 35100;
Best Local Similarity 50.0%; Pred. No. 1.8;
Matches 122; Conservative 0; Mismatches 118; Indels 4; Gaps 1;

QY 2 GGGCGGGAGAGCGCGCGAGAGGAGGCTGATGTCCTCGCGCCTCCACCTCCCGAGGC 61
DB 24529 GCGCCGGCAGACACCCGAGAGCCCGCGCAGACACCCGAGAGCCCGCGCAGACACCCAGGA 24588
QY 62 GCAGAGGCGCCGACAGAGACCCCGAGAGCTGCGACGTTGCGACGTTGCGATTCAGAGGC 121
DB 24589 GCGCCGGCAGACACCCGAGAGCCCGCGCAGACACCCCTCCCGAGAGGGGATCCCGGCGC 24648
QY 122 ----AGGAGCAGAGGAGCCAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 177
DB 24649 GCCACCTCTCCCGAGAGGGGATCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 24708
QY 178 GCTCCCTCACGAGAGGAACTCCCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 237
DB 24709 GCCACCTCTCCCGAGAGGGGATCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 24768
QY 238 GTCA 241
DB 24769 GCCA 24772

RESULT 19
US-08-757-669A-17
; Sequence 17, Application US/08757669A
; Patent No. 6183751
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,669A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-757-669A-17

Query Match          15.0%; Score 37.8; DB 3; Length 35100;
Best Local Similarity 50.0%; Pred. No. 1.8;
Matches 122; Conservative 0; Mismatches 118; Indels 4; Gaps 1;

QY 2 GGGCGGGAGAGCGCGCGAGAGGAGGCTGATGTCCTCGCGCCTCCACCTCCCGAGGC 61
DB 24529 GCGCCGGCAGACACCCGAGAGCCCGCGCAGACACCCGAGAGCCCGCGCAGACACCCAGGA 24588
QY 62 GCAGAGGCGCCGACAGAGACCCCGAGAGCTGCGACGTTGCGACGTTGCGATTCAGAGGC 121
DB 24589 GCGCCGGCAGACACCCGAGAGCCCGCGCAGACACCCCTCCCGAGAGGGGATCCCGGCGC 24648
QY 122 ----AGGAGCAGAGGAGCCAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 177
DB 24649 GCCACCTCTCCCGAGAGGGGATCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 24708
QY 178 GCTCCCTCACGAGAGGAACTCCCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 237
DB 24709 GCCACCTCTCCCGAGAGGGGATCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 24768
QY 238 GTCA 241
DB 24769 GCCA 24772

RESULT 20
US-09-230-371A-17
; Sequence 17, Application US/09230371A
; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,371A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US97/13346
; PRIOR FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 17
; LENGTH: 35100
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
; US-09-230-371A-17
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Query Match 15.0%; Score 37.8; DB 4; Length 35100;  
Best Local Similarity 50.0%; Pred. No. 1.8;  
Matches 122; Conservative 0; Mismatches 118; Indels 4; Gaps 1;

QY 2 GGGCGGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 61  
DB GCGCGGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 24588  
QY 62 GCAGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 121  
DB GCGCGGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 24648  
QY 122 ----AGGAGCGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 177  
DB GCGCGGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 24708  
QY 178 GCTCCCTCACTGAGAGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 24708  
DB GCGCGGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 24708  
QY 238 GTCA 241  
DB 24709 GCGCGGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 24768  
QY 24769 GCGC 24772  
DB 24769 GCGC 24772

RESULT 21  
US-08-466-583-1/c  
; Sequence 1, Application US/08466583  
; Patent No. 591998

GENERAL INFORMATION:  
APPLICANT: Bandurski, Robert S.  
APPLICANT: Szelesen, Jędrzej B.  
TITLE OF INVENTION: Genetic Control of Plant Hormone Levels  
TITLE OF INVENTION: and Plant Growth.  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Greenlee & Winney, P. C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: United States of America  
ZIP: 80303

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,583  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 800

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/265,427  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Feiber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 11-94A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/499-8080  
TELEFAX: 303/499-8089  
TELEX: 49617824

INFORMATION FOR SEQ. ID NO. 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1731 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 57..1472

US-08-466-583-1  
Query Match 14.9%; Score 37.6; DB 2; Length 1731;  
Best Local Similarity 51.7%; Pred. No. 1.8;  
Matches 108; Conservative 0; Mismatches 100; Indels 1; Gaps 1;

QY 5 CGGAGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 64  
DB CCGGAGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 1346  
QY 65 GAGAGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 124  
DB GAGAGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 1287  
QY 125 GAGAGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 184  
DB GAGAGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 1227  
QY 185 CAGCAGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 213  
DB 1226 GTTCGAGAGCGCGGAGTGGAGCTGATGCTCCCTGGCGCTCCCACTCCCGAGC 1198

RESULT 22  
US-08-265-427-1/c  
; Sequence 1, Application US/08265427  
; Patent No. 6489541

GENERAL INFORMATION:  
APPLICANT: Bandurski, Robert S.  
APPLICANT: Szelesen, Jędrzej B.  
TITLE OF INVENTION: Genetic Control of Plant Hormone Levels  
TITLE OF INVENTION: and Plant Growth.  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Greenlee & Winney, P. C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: United States of America  
ZIP: 80303

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/265,427  
FILING DATE: June 24, 1994  
CLASSIFICATION: 800

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/265,427  
FILING DATE: 24-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Feiber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 11-94  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/499-8080  
TELEFAX: 303/499-8089  
TELEX: 49617824

INFORMATION FOR SEQ. ID NO. 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1731 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 57..1472  
Query Match 14.9%; Score 37.6; DB 4; Length 1731;  
Best Local Similarity 51.7%; Pred. No. 1.8;  
Matches 108; Conservative 0; Mismatches 100; Indels 1; Gaps 1;













REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 760100.418C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1120 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-030-613-1

Query Match 14.2%; Score 35.8; DB 3; Length 1120;  
Best Local Similarity 47.0%; Pred. No. 4.6;  
Matches 109; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 2 GCGCGGAGAGCGCGCGAGTGTGATGCTCCCTGCGCGCTCCACCTCCCGAGGC 61  
DB 452 GGTCTTGAAGTGTGCGCGCGGAGAGCCGCGCTGCGCGCATCTCGGCGCAAGCGCGC 393  
QY 62 GCAGAGGCGCGCCACAGAGAGCCCGAGTGTGCGCGCGTGTGCGATCAGAGGC 121  
DB 392 AGCGTGTATGTCTCCGCGTGTGATGTCTGCGGCGCGCGCGCGGATCCCGAGGC 333  
QY 122 AGGACACAGAGAGCGAGAACTGTGCGCGCGCGCGCGCGCGCTGTGCGAGAGAGCTC 181  
DB 332 GCTGAGAGCGCGCGCGGAGCGCGCTGTCCCGCGCGCGCGCGCGCTCCAGCGCGCTC 273  
QY 182 CCTCACACAGAGAGAACTCCCTCACCGCGCGCGCGCGCGCGCGCGCGCGCG 233  
DB 272 CGGCGACAGCG 221

RESULT 38  
US-09-451-905-1/c  
Sequence 1, Application US/09451905  
Patent No. 6306613  
GENERAL INFORMATION:  
APPLICANT: Robert Z. Florkiewicz  
APPLICANT: Andrew Balid  
TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT  
TITLE OF INVENTION: AND METHODS FOR IDENTIFYING AND USING THE SAME  
FILE REFERENCE: 200124.402C4  
CURRENT APPLICATION NUMBER: US/09/451,905  
CURRENT FILING DATE: 1999-12-01  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1120  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-451-905-1

Query Match 14.2%; Score 35.8; DB 4; Length 1120;  
Best Local Similarity 47.0%; Pred. No. 4.6;  
Matches 109; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 2 GCGCGGAGAGCGCGCGAGTGTGATGCTCCCTGCGCGCTCCACCTCCCGAGGC 61  
DB 452 GGTCTTGAAGTGTGCGCGCGGAGAGCCGCGCTGCGCGCATCTCGGCGCAAGCGCGC 393  
QY 62 GCAGAGGCGCGCCACAGAGAGCCCGAGTGTGCGCGCGTGTGCGATCAGAGGC 121  
DB 392 AGCGTGTATGTCTCCGCGTGTGATGTCTGCGGCGCGCGCGCGGATCCCGAGGC 333  
QY 122 AGGACACAGAGAGCGAGAACTGTGCGCGCGCGCGCGCGCGCTGTGCGAGAGAGCTC 181  
DB 332 GCTGAGAGCGCGCGCGGAGCGCGCTGTCCCGCGCGCGCGCGCGCTCCAGCGCGCTC 273  
QY 182 CCTCACACAGAGAGAACTCCCTCACCGCGCGCGCGCGCGCGCGCGCGCGCG 233

DB 272 CGGCGACAGCG 221

RESULT 39  
US-09-595-549-1/c  
Sequence 1, Application US/09595549  
Patent No. 6511827  
GENERAL INFORMATION:  
APPLICANT: Howard, Andrew D.  
APPLICANT: Casclieri, Margaret A.  
APPLICANT: Smith, Roy G.  
APPLICANT: Sullivan, Kathleen A.  
APPLICANT: Tan, Carina  
APPLICANT: Van der Ploeg, Leonardus H. T.  
TITLE OF INVENTION: GALANIN RECEPTOR GALR3 AND NUCLEOTIDES  
TITLE OF INVENTION: ENCODING SAME  
FILE REFERENCE: 20148PCA  
CURRENT APPLICATION NUMBER: US/09/595,549  
CURRENT FILING DATE: 2000-06-16  
PRIOR APPLICATION NUMBER: US98/26812  
PRIOR FILING DATE: 1998-12-17  
PRIOR APPLICATION NUMBER: 60/069,725  
PRIOR FILING DATE: 1997-12-17  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 2263  
TYPE: DNA  
ORGANISM: human  
US-09-595-549-1

Query Match 14.1%; Score 35.6; DB 4; Length 2263;  
Best Local Similarity 49.7%; Pred. No. 5.2;  
Matches 83; Conservative 2; Mismatches 82; Indels 0; Gaps 0;

QY 37 CCTGCGCGCTCCACCTCCCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 96  
DB 1731 CYTTGGTGTGCG 1672  
QY 97 GTTCCACGCTGTGAGATCAGAGAGCGAGAGCGAGAGCGAGAGAGCGAGAGAGCTCCCGC 156  
DB 1671 CGTAGGCGAGGCTCACACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1612  
QY 157 CCTGCGCGCGCGCGAGAGAGCTCCCTCACCGAGAGAGAGAGAGAGAGAGAGAGCTCCCGC 203  
DB 1611 CCAGGCG 1565

RESULT 40  
US-09-103-840A-1/c  
Sequence 1, Application US/09103840A  
Patent No. 6294328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
TITLE OF INVENTION: TUBERCULOSIS  
FILE REFERENCE: 24366-20007.00  
CURRENT APPLICATION NUMBER: US/09/103,840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 4411529  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
OTHER INFORMATION: H37RV  
US-09-103-840A-1

Query Match 14.1%; Score 35.6; DB 3; Length 4411529;



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Db 61 CGCAGAAAGGCGCCCGACAGAGAGAGCCCGACGTCGACGCTGTGGATCAGAGG 120  
Qy 121 CAGGAGACGAGGAGCGCAGAACTGCGCGCGCCCGCCCTGCGCGAGGAGAGCT 180  
Db 121 CAGGAGACGAGGAGCGCAGAACTGCGCGCGCCCGCCCTGCGCGAGGAGCT 177  
Qy 181 CCCCTCACGCGAGGAGGAGTCCCTTCCACCGCGCGCGCGCGCGCGCGCGCTG 240  
Db 178 CCCCTCACGCGAGGAGGAGTCCCTTCCACCGCGCGCGCGCGCGCGCGCTG 236  
Qy 241 AGACCGGAAAGC 252  
Db 237 AGACCGGAAAGC 248

RESULT 2  
US-10-027-632-196114/c  
Sequence 196114, Application US/10027632  
Publication No. US20030204075A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/1218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 196114  
LENGTH: 533  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-196114

Query Match 57.0%; Score 143.6; DB 12; Length 533;  
Best Local Similarity 94.8%; Pred. No. 4.1e-26;  
Matches 181; Conservative 0; Mismatches 5; Indels 5; Gaps 3;  
Qy 1 CGGCGGAGGAGCGCGCGGAGTGAGGCTGATGCTCCCTGCGCGCTCCACCTCCCAAG 60  
Db 189 CGGCGGAGGAGCGCGCGGAGTGAGGCTGATGCTCCCTGCGCGCTCCACCTCCCAAG 130  
Qy 61 CGCAGAGGCGCCCGACAGAGAGCCCGACGTCGCGCGAGCTTGCACGCTTGGATCAGAG 120  
Db 129 CGCAGAGGCGCCCGACAGAGAGCCCGACGTCGCGCGAGCTTGCACGCTTGGATCAGAG 70  
Qy 121 CA-GGAGACGAGGAGCGCAGAACTGCGCGCGCGCGCGCGCGCGCGCTGCGCGAGGAG 179  
Db 69 CAGGAGACGAGGAGCGCAGAACTGCGCGCGCGCGCGCGCGCGCGCTGCGCGAG-GGAGC 14  
Qy 180 TCCTCTACCGG 190  
Db 13 TCCTCTACCGG 3

RESULT 3  
US-10-027-632-196114/c  
Sequence 196114, Application US/10027632  
GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 196114  
LENGTH: 533  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-196114

Query Match 57.0%; Score 143.6; DB 13; Length 533;  
Best Local Similarity 94.8%; Pred. No. 4.1e-26;  
Matches 181; Conservative 0; Mismatches 5; Indels 5; Gaps 3;  
Qy 1 CGGCGGAGGAGCGCGCGGAGTGAGGCTGATGCTCCCTGCGCGCTCCACCTCCCAAG 60  
Db 189 CGGCGGAGGAGCGCGCGGAGTGAGGCTGATGCTCCCTGCGCGCTCCACCTCCCAAG 130  
Qy 61 CGCAGAGGCGCCCGACAGAGAGCCCGACGTCGCGCGAGCTTGCACGCTTGGATCAGAG 120  
Db 129 CGCAGAGGCGCCCGACAGAGAGCCCGACGTCGCGCGAGCTTGCACGCTTGGATCAGAG 70  
Qy 121 CA-GGAGACGAGGAGCGCAGAACTGCGCGCGCGCGCGCGCGCGCGCTGCGCGAGGAG 179  
Db 69 CAGGAGACGAGGAGCGCAGAACTGCGCGCGCGCGCGCGCGCGCGCTGCGCGAG-GGAGC 14  
Qy 180 TCCTCTACCGG 190  
Db 13 TCCTCTACCGG 3

RESULT 4  
US-10-059-579-120  
Sequence 120, Application US/10059579  
Publication No. US20030138783A1  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
APPLICANT: SUKUMAR, Saraswati  
APPLICANT: EVRON, Ella  
APPLICANT: DOOLEY, William C.  
APPLICANT: DAVIDSON, Nancy  
APPLICANT: FACKLER, Mary Jo.  
TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY  
FILE REFERENCE: JHU1630-1  
CURRENT APPLICATION NUMBER: US/10/059,579  
PRIOR FILING DATE: 2003-02-03  
PRIOR APPLICATION NUMBER: US 09/771,357  
PRIOR FILING DATE: 2001-01-26  
NUMBER OF SEQ ID NOS: 136  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 120  
LENGTH: 1794  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:







Db 7676 CGCGGAGGAGCGCGCGCGCGCGCGCGAGAGCTCGGAGCGGAGCGCGCGCGCGCGCG 7617  
Qy 61 CGCAGAGAGCG 120  
Db 7616 GCG 7557  
Qy 121 CAGGAGACCGAGGAGCG 180  
Db 7556 TCGCCGCT 7497  
Qy 181 CCTACACGAGGAGCG 217  
Db 7496 CCGCT 7460

RESULT 12  
US-09-836-911A-17/c  
; Sequence 17, Application US/09936911A  
; Publication No. US2003003617A1

GENERAL INFORMATION:  
APPLICANT: Hadlaczky, Gyula  
Szalay, Aladar

TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF  
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES

NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Erman White & McAniff  
STREET: 4350 La Jolla Village Drive, 6th Floor  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION NUMBER: US/09/836,911A  
PENDING DATE: 17-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIORITY INFORMATION: <Unknown>

APPLICATION NUMBER: 08/835,682  
FILING DATE: 10-Apr-1997  
APPLICATION NUMBER: 08/695,191  
FILING DATE: 07-Aug-1996  
APPLICATION NUMBER: 08/682,080  
FILING DATE: 15-Jul-1996  
APPLICATION NUMBER: 08/629,822  
FILING DATE: 10-Apr-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 24601-4021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858-450-8403  
TELEFAX: 858-587-5360  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4299 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOETHERICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-836-911A-17

Query Match 15.2%; Score 38.4; DB 11; Length 42999;

Best Local Similarity 48.4%; Pred. No. 0.35;  
Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;  
Qy 1 CGCGGAGGAGCGCGCGCGCGCGCGCGAGAGCTCGGAGCGGAGCGCGCGCGCGCGCG 60  
Db 7676 CGCGGAGGAGCG 7617  
Qy 61 CGCAGAGAGCG 120  
Db 7616 GCG 7557  
Qy 121 CAGGAGACCGAGGAGCG 180  
Db 7556 TCGCCGCT 7497  
Qy 181 CCTACACGAGGAGCG 217  
Db 7496 CCGCT 7460

RESULT 13  
US-09-738-630-73/c  
; Sequence 73, Application US/09738630  
; Publication No. US2003016621A1

GENERAL INFORMATION:  
APPLICANT: Greenpan, Ralph J.  
Shaw, Paul J.

TITLE OF INVENTION: Methods For Identifying Compounds That  
Modulate Disorders Related To Nitric Oxide/CGMP-Dependent  
FILE REFERENCE: P-NI 3906  
CURRENT APPLICATION NUMBER: US/09/738,630  
PENDING FILING DATE: 2000-12-15  
NUMBER OF SEQ ID NOS: 105  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 73

LENGTH: 42999  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(42999)  
OTHER INFORMATION: n = A,T,C or G  
US-09-738-630-73

Query Match 15.2%; Score 38.4; DB 12; Length 42999;  
Best Local Similarity 48.4%; Pred. No. 0.35;  
Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Qy 1 CGCGGAGGAGCGCGCGCGCGCGCGCGAGAGCTCGGAGCGGAGCGCGCGCGCGCGCG 60  
Db 7676 CGCGGAGGAGCG 7617  
Qy 61 CGCAGAGAGCG 120  
Db 7616 GCG 7557  
Qy 121 CAGGAGACCGAGGAGCG 180  
Db 7556 TCGCCGCT 7497  
Qy 181 CCTACACGAGGAGCG 217  
Db 7496 CCGCT 7460

RESULT 14  
US-10-125-767-17/c  
; Sequence 17, Application US/10125767  
; Publication No. US20020160410A1  
GENERAL INFORMATION:  
APPLICANT: Hadlaczky, Gyula  
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND

METHODS  
FOR PREPARING ARTIFICIAL CHROMOSOMES

NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McCauliffe LLP  
STREET: 4350 La Jolla Village Drive, 7th Floor  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/125,767  
FILING DATE: 17-Apr-2002

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/724,693  
FILING DATE: 28-NOV-2000  
APPLICATION NUMBER: 08/835,682  
FILING DATE: 10-APR-1997  
APPLICATION NUMBER: 08/695,191  
FILING DATE: 07-AUG-1996  
APPLICATION NUMBER: 08/682,080  
FILING DATE: 15-JUL-1996  
APPLICATION NUMBER: 08/629,822  
FILING DATE: 10-APR-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 24601-402J  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858-450-8403  
TELEFAX: 858-587-5360  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4299 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-10-125-767-17

Query Match 15.2%; Score 38.4; DB 13; Length 42999;  
Best Local Similarity 48.4%; Pred. No. 0.35;  
Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 1 CGGCGGAGGAGGCGGCGGAGGAGGCTGATGCTCCCTGCGGCGCTCCACCTCCCGCAGG 60  
DB 7676 CGGCGGAGGAGGCGGCGGAGGAGGCTGATGCTCCCTGCGGCGCTCCACCTCCCGCAGG 7617

QY 61 CGCAGAGAGGCGCCAGAGAGAGCCCGGAGGCTTGCACAGGCTCTGGATCAGAGG 120  
DB 7616 GCGGCGGCGGAGGCGGAGGAGGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGG 7557

QY 121 CAGGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
DB 7556 TCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7497

QY 181 CCGTCACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 217  
DB 7496 CCGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7460

RESULT 15

US-10-151-081-17/C

Sequence 17, Application US/10151081  
Publication No. US20030083293A1  
GENERAL INFORMATION:  
APPLICANT: Hadjaczky, Gyula  
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF  
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES

NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McCauliffe  
STREET: 4250 Executive Square, 7th Floor  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/151,081  
FILING DATE: 16-May-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/799,462  
FILING DATE: HEREWITH 05-MAR-2001  
APPLICATION NUMBER: 09/724,693  
FILING DATE: HEREWITH 28-NOV-2000  
APPLICATION NUMBER: 08/835,682  
FILING DATE: 07-AUG-1996  
APPLICATION NUMBER: 08/695,191  
FILING DATE: 15-JUL-1996  
APPLICATION NUMBER: 08/682,080  
FILING DATE: 10-APR-1996  
APPLICATION NUMBER: 08/629,822  
FILING DATE: 10-APR-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 24601-402L  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858-450-8403  
TELEFAX: 858-587-5360  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4299 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-10-151-081-17

Query Match 15.2%; Score 38.4; DB 14; Length 42999;  
Best Local Similarity 48.4%; Pred. No. 0.35;  
Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 1 CGGCGGAGGAGGCGGCGGAGGAGGCTGATGCTCCCTGCGGCGCTCCACCTCCCGCAGG 60  
DB 7676 CGGCGGAGGAGGCGGCGGAGGAGGCTGATGCTCCCTGCGGCGCTCCACCTCCCGCAGG 7617

QY 61 CGCAGAGAGGCGCCAGAGAGAGCCCGGAGGCTTGCACAGGCTCTGGATCAGAGG 120  
DB 7616 GCGGCGGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7557

QY 121 CAGGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180





Query Match 15.2%; Score 38.4; DB 14; Length 42999;  
Best Local Similarity 48.4%; Pred. No. 0.35; Mismatches 112; Indels 0; Gaps 0;  
Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 1 CGGCGGAGAGCGCGCGGAGTGTAGCTGATCGTCTGCGGCTTCACTCCCGAG 60  
DB 7676 CGGCGGAGAGCGCGCGGAGTGTAGCTGATCGTCTGCGGCTTCACTCCCGAG 7617  
QY 61 CGGAGAGGCGCGCGGAGAGAGCGCGGAGTGTAGCTGATCGTCTGCGGCTTCACTCCCGAG 120  
DB 7616 CGGCGGAGAGCGCGCGGAGAGAGCGCGGAGTGTAGCTGATCGTCTGCGGCTTCACTCCCGAG 7557  
QY 121 CAGGAGCAG 180  
DB 7556 TCCCGCGGAG 7497  
QY 181 CCTCACAG 217  
DB 7496 CCGGCGGAG 7460

RESULT 18  
US-10-125-815-4/c  
; Sequence 4; Application US/10125815  
; Publication No. US20020173008A1  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Zhihao  
; APPLICANT: McDaniel, Robert  
; APPLICANT: Sant, Daniel V.  
; TITLE OF INVENTION: RECOMBINANT POLYKETIDE SYNTHASE GENES  
; FILE REFERENCE: 30062204720  
; CURRENT FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: 09/679,279  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: 60/190,024  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/158,305  
; PRIOR FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 615  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: megks6  
US-10-125-815-4

Query Match 15.2%; Score 38.2; DB 13; Length 615;  
Best Local Similarity 48.2%; Pred. No. 1.1; Mismatches 114; Indels 0; Gaps 0;  
Matches 106; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 14 GGGCGGAG 73  
DB 299 GGGCGGAG 240  
QY 74 CAGGAG 133  
DB 239 CAGGAG 180  
QY 134 CAGGAG 193  
DB 179 GAGTCCGAG 120  
QY 194 GAGTCCGAG 233  
DB 119 CTGGCGAG 80

RESULT 19  
US-10-156-761-6400/c  
; Sequence 6400; Application US/10156761

Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIGAWA, YUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 6400  
; LENGTH: 1365  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1365)  
US-10-156-761-6400

Query Match 15.2%; Score 38.2; DB 14; Length 1365;  
Best Local Similarity 47.8%; Pred. No. 0.91; Mismatches 119; Indels 0; Gaps 0;  
Matches 109; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 1 CGGCGGAG 60  
DB 244 CGGCGGAG 185  
QY 61 CGGAGAGGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
DB 184 CGGAGAGGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 125  
QY 121 CAGGAGCAG 180  
DB 124 CGGCGGAG 65  
QY 181 CCTCACAG 228  
DB 64 CCGCGGAG 17

RESULT 20  
US-10-020-079-11  
; Sequence 11; Application US/10020079  
; Publication No. US20020161213A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Fridde, Carl Johan  
; TITLE OF INVENTION: NO US20020161213A1 Human Kinases and Polynucleotides Encoding  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2001-05-08  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 1947  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-11

Query Match 15.0%; Score 37.8; DB 13; Length 1947;

Best Local Similarity 50.6%; Pred. No. 1;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 35 GTCCCTGAGGCTTCACCTCCCGAGAGGCGCCCGACGAGACCCCGATGCCG 94  
Db 41 GCGGCTGCTCCCGCCCGCTGCTCCCAAGAGATCGGGCCGGCCCGGATGATCCG 100  
QY 95 ACCTTGCCACGCTCTGGATCAGAGCAGAGACCAAGAGCCAGAACTGCCCGCCG 154  
Db 101 GTGGAAGGCGCGCGCGCGCGGAGGAGGCTCACCCAGCCGCACTGAGCGCCG 160  
QY 155 GCGGCTGCTGCGCGCGAGGAAAGCTTCACACNAGAGAACTCCCTCACCGCGC 212  
Db 161 GCGCGCGCGCGCGCGGAGATGCGCGCCGAGCTGCTGCGCGCGCGCGC 218

RESULT 21  
US-10-020-079-9  
; Sequence 9, Application US/10020079  
; Publication No. US20020161213A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; TITLE OF INVENTION: No. US20020161213A1 Human Kinases and Polynucleotides Encoding  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1965  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-9

Query Match 15.0%; Score 37.8; DB 13; Length 1965;  
Best Local Similarity 50.6%; Pred. No. 1;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 35 GTCCCTGAGGCTTCACCTCCCGAGAGGCGCCCGACGAGACCCCGATGCCG 94  
Db 59 GCGGCTGCTCCCGCCCGCTGCTCCCAAGAGATCGGGCCGGCCCGGATGATCCG 118  
QY 95 ACCTTGCCACGCTCTGGATCAGAGCAGAGACCAAGAGCCAGAACTGCCCGCCG 154  
Db 119 GTGGAAGGCGCGCGCGCGGAGGAGCGGCTCACCCAGCCGCACTGAGCGCCG 178  
QY 155 GCGGCTGCTGCGCGCGAGGAAAGCTTCACACNAGAGAACTCCCTCACCGCGC 212  
Db 179 GCGCGCGCGCGCGCGGAGATGCGCGCCGAGCTGCTGCGCGCGCGCGC 236

RESULT 22  
US-10-020-079-3  
; Sequence 3, Application US/10020079  
; Publication No. US20020161213A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; TITLE OF INVENTION: No. US20020161213A1 Human Kinases and Polynucleotides Encoding  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; PRIOR FILING DATE: 2001-05-08

NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 2595  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-3

Query Match 15.0%; Score 37.8; DB 13; Length 2595;  
Best Local Similarity 50.6%; Pred. No. 0.97;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 35 GTCCCTGAGGCTTCACCTCCCGAGAGGCGCCCGACGAGACCCCGATGCCG 94  
Db 41 GCGGCTGCTCCCGCCCGCTGCTCCCAAGAGATCGGGCCGGCCCGGATGATCCG 100  
QY 95 ACCTTGCCACGCTCTGGATCAGAGCAGAGACCAAGAGCCAGAACTGCCCGCCG 154  
Db 101 GTGGAAGGCGCGCGCGCGGAGGAGGCTCACCCAGCCGCACTGAGCGCCG 160  
QY 155 GCGGCTGCTGCGCGCGAGGAAAGCTTCACACNAGAGAACTCCCTCACCGCGC 212  
Db 161 GCGCGCGCGCGCGCGGAGATGCGCGCCGAGCTGCTGCGCGCGCGCGC 218

RESULT 23  
US-10-020-079-1  
; Sequence 1, Application US/10020079  
; Publication No. US20020161213A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; TITLE OF INVENTION: No. US20020161213A1 Human Kinases and Polynucleotides Encoding  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2613  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-1

Query Match 15.0%; Score 37.8; DB 13; Length 2613;  
Best Local Similarity 50.6%; Pred. No. 0.97;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 35 GTCCCTGAGGCTTCACCTCCCGAGAGGCGCCCGACGAGACCCCGATGCCG 94  
Db 59 GCGGCTGCTCCCGCCCGCTGCTCCCAAGAGATCGGGCCGGCCCGGATGATCCG 118  
QY 95 ACCTTGCCACGCTCTGGATCAGAGCAGAGACCAAGAGCCAGAACTGCCCGCCG 154  
Db 119 GTGGAAGGCGCGCGCGCGGAGGAGGCTCACCCAGCCGCACTGAGCGCCG 178  
QY 155 GCGGCTGCTGCGCGCGAGGAAAGCTTCACACNAGAGAACTCCCTCACCGCGC 212  
Db 179 GCGCGCGCGCGCGCGGAGATGCGCGCCGAGCTGCTGCGCGCGCGCGC 236

RESULT 24  
US-10-020-079-19  
; Sequence 19, Application US/10020079  
; Publication No. US20020161213A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian



Db	5	GCCGCTGCGCGCCGCTCTCCGCCAAGGAGATCGGGGCGGGGCGGGGCGGGATGATCCGG	118
Qy	95	ACGTTGCACCGCTCTGGATCATGAGGCAGGGGACCGAGGATCTGGCGCGCGCCC	154
Db	119	GTCGGAGAGCGCGCGCGCGCGGAGGAGGGGTATCCACGCGCGCATGACCGCGCCC	178
Qy	155	GCCCCCTGCGCTGGCGGGAGAGAAAGTCTCTACACGAGGAAAGTCTCCCTTACCCGGC	212
Db	179	GCCCCCGCCCGGCGGGGAGATGGCGCGCCCGGAGCTGCTGCTCGCGCGCGCGCGC	236

APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 4416  
LENGTH: 2316  
TYPE: DNA  
ORGANISM: Streptomyces avermitilis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(2316)  
US-10-156-761-4416

Query Match 14.8%; Score 37.4; DB 14; Length 2316;  
Best Local Similarity 50.3%; Pred. No. 1.3;  
Matches 89; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 14 GGCGGGAGTGAAGCTGATCTGCTGCGGCTCCCACTCCCGAGCGGAGAGGCGCC 73  
DB 1174 GGCGTGCAGACACACAGCTGCGGAGTGTGGAGCGCCGAGCCGCGCGGCGCGCC 1233  
QY 74 CACGAGAGCCCGAGTGCAGCGTGGCCAGCGTGTGGATCAGAGGACGAGGAGGA 133  
DB 1234 CTCGAGAGACACACAGGATCCCGGTCGCTTGCACACCGTGCAGGAGGAGGAG 1293  
QY 134 GCGAGAGTGCAGCG 188  
DB 1294 CTGTGTGTCTGCG 1348

RESULT 32  
US-09-918-995-27197/c  
Sequence 27197, Application US/09918995  
Publication No. US20030073623A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc.  
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
FILE REFERENCE: 20411-756  
CURRENT APPLICATION NUMBER: US/09/918,995  
CURRENT FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: US/09/235,076  
PRIOR FILING DATE: 1999-01-20  
NUMBER OF SEQ ID NOS: 38054  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 27197  
LENGTH: 528  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(528)  
OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-27197

Query Match 14.8%; Score 37.2; DB 11; Length 528;  
Best Local Similarity 50.3%; Pred. No. 2;  
Matches 90; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 69 GGCGCCGAGGAGCCCGGAGTGCAGCGTGGCCAGCGTGTGGATCAGAGGAGGAGGAGC 128  
DB 385 GGCGCCGAGGAGCCCGGAGTGCAGCGTGGCCAGCGTGTGGATCAGAGGAGGAGGAGC 326  
QY 129 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 188

DB 325 GAAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 266  
QY 189 NGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 247  
DB 265 AAAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 207

RESULT 33  
US-10-029-386-7001  
Sequence 7001, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
FILE REFERENCE: AEWICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1  
SEQ ID NO 7001  
LENGTH: 526  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC004080.1, SIGNAL = 3.4  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4  
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.8  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8  
OTHER INFORMATION: NT HIT: US2827.1, EVALUATE 0.006+00  
OTHER INFORMATION: SWISSPROT HIT: P31271, EVALUATE 3.006-23  
OTHER INFORMATION: EST\_HUMAN HIT: AA160421.1, EVALUATE 8.006-41  
US-10-029-386-7001

Query Match 14.7%; Score 37; DB 12; Length 526;  
Best Local Similarity 51.9%; Pred. No. 2.2;  
Matches 82; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 88 GTGCCGAGGAGTGCAGCGTGTGGATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 147  
DB 120 GTGCCGAGGAGTGCAGCGTGTGGATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 179  
QY 148 CGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 207  
DB 180 AAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 239  
QY 208 CCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 245  
DB 240 CCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 277

RESULT 34  
US-10-156-761-4189  
Sequence 4189, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 4189  
LENGTH: 4437  
TYPE: DNA  
ORGANISM: Streptomyces avermitilis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(4437)  
US-10-156-761-4189

Query Match 14.5%; Score 36.6; DB 14; Length 4437;  
Best Local Similarity 51.2%; Pred. No. 1.7; Mismatches 0; Gaps 0;  
Matches 84; Conservative 0; Indels 80; Gaps 0;

QY 84 CCCAGTCCCGAGCTTCCGATCTGATCAGAGGACGAGGACCGAGGACT 143  
DB 3428 CCCAGAGCGGAGCCTCTCCGCGACCAACGAGCTGAGGCGCGAGCTCG 3487  
QY 144 GCGCGCCCGCCCTGCTGCGCGAGGAGGAGCTCTCAACGAGGAGCTCC 203  
DB 3488 GCACCTCTCCGAGCCCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAG 3547  
QY 204 TCACCGCGAGCGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 247  
DB 3548 CCGGCGAGTCCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3591

RESULT 35  
US-09-769-734-49/c  
Sequence 49, Application US/09769734  
Publication No. US20030143666A1  
GENERAL INFORMATION:  
APPLICANT: Ecopia Biosciences Inc.  
TITLE OF INVENTION: Genetic Locus for Evernimycin Biosynthesis  
FILE REFERENCE: PA 005-US  
CURRENT APPLICATION NUMBER: US/09/769,734  
CURRENT FILING DATE: 2001-01-26  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: PatentIn Version 3.0  
SEQ ID NO 49  
LENGTH: 11115  
TYPE: DNA  
ORGANISM: M. carbonacei  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (8)..(1207)  
OTHER INFORMATION: ORF 41 (positive strandedness)  
OTHER INFORMATION: Incomplete: C-terminus only  
NAME/KEY: misc\_feature  
LOCATION: (1213)..(2331)  
OTHER INFORMATION: ORF 42 (positive strandedness)  
NAME/KEY: misc\_feature  
LOCATION: (2364)..(3611)  
OTHER INFORMATION: ORF 43 (positive strandedness)  
NAME/KEY: misc\_feature  
LOCATION: (3623)..(4243)  
OTHER INFORMATION: ORF 44 (positive strandedness)  
NAME/KEY: misc\_feature  
LOCATION: (4145)..(5177)  
OTHER INFORMATION: ORF 45 (positive strandedness)  
NAME/KEY: misc\_feature  
LOCATION: (5177)..(6094)  
OTHER INFORMATION: ORF 46 (negative strandedness)  
NAME/KEY: misc\_feature  
LOCATION: (6271)..(7824)  
OTHER INFORMATION: ORF 47 (negative strandedness)  
NAME/KEY: misc\_feature  
LOCATION: (7903)..(8760)  
OTHER INFORMATION: ORF 48 (negative strandedness)  
NAME/KEY: misc\_feature

LOCATION: (8781)..(9800)  
OTHER INFORMATION: ORF 49 (negative strandedness)  
US-09-769-734-49

Query Match 14.5%; Score 36.6; DB 12; Length 11115;  
Best Local Similarity 50.3%; Pred. No. 1.3; Mismatches 89; Indels 0; Gaps 0;  
Matches 90; Conservative 0; Indels 89; Gaps 0;

QY 1 CGGCGGAGGAGGCGGCGGAGTGAAGCTGATGCTCCCTGAGGCTCCACCTCCAG 60  
DB 8173 CGGCTGAGAGTGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8114  
QY 61 CGCAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
DB 8113 CTGGAGGAGCTTCAGCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 8054  
QY 121 CAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 179  
DB 8053 CGTGACGAGTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7995

RESULT 36  
US-10-187-900-3  
Sequence 3, Application US/10187900  
Publication No. US20030166221A1  
GENERAL INFORMATION:  
APPLICANT: BEASLEY, Ellen M. et al  
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
FILE REFERENCE: CL001061  
CURRENT APPLICATION NUMBER: US/10/187,900  
CURRENT FILING DATE: 2002-07-03  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 16389  
TYPE: DNA  
ORGANISM: Human  
US-10-187-900-3

Query Match 14.5%; Score 36.6; DB 12; Length 16389;  
Best Local Similarity 48.1%; Pred. No. 1.2; Mismatches 110; Indels 0; Gaps 0;  
Matches 102; Conservative 0; Indels 110; Gaps 0;

QY 2 GCGCGGAGGAGGCGGCGGAGTGAAGCTGATGCTCCCTGAGGCTCCACCTCCAGGC 61  
DB 12683 GCGTGGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 12742  
QY 62 GCAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 121  
DB 12743 CCAGGAGGAGTGAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 12802  
QY 122 AGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 181  
DB 12803 TGTACATTGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 12862  
QY 182 CCTACGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 213  
DB 12863 ACGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 12894

RESULT 37  
US-10-027-632-9421/c  
Sequence 9421, Application US/10027632  
Publication No. US20030204075A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
TITLE OF INVENTION: Polymorphisms in the Human Genome  
FILE REFERENCE: 108927.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30

```
; ORGANISM: Human
; US-10-027-632-9422
Query Match
Best Local Similarity 49.2%; Pred. No. 2.6;
Matches 91; Conservative 1; Mismatches 93; Indels 0; Gaps 0;

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9422
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-9421

Query Match
Best Local Similarity 14.4%; Score 36.4; DB 12; Length 1114;
Matches 91; Conservative 1; Mismatches 93; Indels 0; Gaps 0;

QY 16 CCGGAGTGAAGGCTGATGCTGCTCCCTGCGCTCCACCTCCCGAGCGCAGAAAGCGCCCA 75
DB 862 CTGCGGCTGTGAGTCTCTCCACAGGGGGCTTGTGAGCCAGGGAGCGAGGTAGTCCC 803
QY 76 CGAGGACCCCAAGTGCCTGCTCCAGCGTCTGGGATCAGAGCGAGGACCGAGGAGC 135
DB 802 CGTCTCCAGCCAGCGAGCGCGCCGACAGAGGGGATCTCCCATCTGCCCCCTCAAG 743
QY 136 CAGGAAGTGGCGCGCCCGCCCTGCGCGCGAGGAGGAGTCTCCCTCACCNGAGGA 195
DB 742 CGGGAATTTTGCTTACGCGCGCGCTCTCCRGAAGAGAGCTCTCCACCTTAAGGC 683
QY 196 AGCTC 200
DB 682 TCCTC 678

RESULT 38
; US-10-027-632-9422/C
; Sequence 9422, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9422
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-9421
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; ORGANISM: Human
; US-10-027-632-9422
Query Match
Best Local Similarity 49.2%; Pred. No. 2.6;
Matches 91; Conservative 1; Mismatches 93; Indels 0; Gaps 0;

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9421
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-9421

Query Match
Best Local Similarity 14.4%; Score 36.4; DB 13; Length 1114;
Matches 91; Conservative 1; Mismatches 93; Indels 0; Gaps 0;

QY 16 CCGGAGTGAAGGCTGATGCTGCTCCCTGCGCTCCACCTCCCGAGCGCAGAAAGCGCCCA 75
DB 862 CTGCGGCTGTGAGTCTCTCCACAGGGGGCTTGTGAGCCAGGGAGCGAGGTAGTCCC 803
QY 76 CGAGGACCCCAAGTGCCTGCTCCAGCGTCTGGGATCAGAGCGAGGACCGAGGAGC 135
DB 802 CGTCTCCAGCCAGCGAGCGCGCCGACAGAGGGGATCTCCCATCTGCCCCCTCAAG 743
QY 136 CAGGAAGTGGCGCGCCCGCCCTGCGCGCGAGGAGGAGTCTCCCTCACCNGAGGA 195
DB 742 CGGGAATTTTGCTTACGCGCGCGCTCTCCRGAAGAGAGCTCTCCACCTTAAGGC 683
QY 196 AGCTC 200
DB 682 TCCTC 678

RESULT 39
; US-10-027-632-9421/C
; Sequence 9421, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9421
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-9421
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Fri Nov 7 08:10:00 2003

us-10-081-817a-19\_copy\_1\_252.rmpb

Page 16

Db 682 TCCTC 678

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RESULT 40
US-10-027-632-9422/c
; Sequence 9422 Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 10827.119
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9422
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-9422
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Query Match 14.4% Score 36.4; DB 13; Length 1114;  
Best Local Similarity 49.2%; Pred No 2.6;  
Matches 91; Conservative 1; Mismatches 93; Indels 0; Gaps 0;

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QY 16 CCGGAGTGGGCTTATGTCCTCGGCTTCCAGGCGGAGAGGCGCCCA 75
DB 862 CTGCGGCTCTGTCCTCTCCACAGGGGCTTCTGAGAGCCAGAGGAGTATGCC 803
QY 76 CGAGAACCCCAAGTCCCAAGTTGCCAGGTCGTGGATCAGAGGAGCCAGGAGC 135
DB 802 CGTCTCCAGCCAGGCGGCGGCGAGAGGAGATCTCCCAATCTGCCCCGTACG 743
QY 136 CAGGAACCTGCGCGCCCGCCCTGAGCGGCGAGGAGAACTTCCCTACCCNAGGGA 195
DB 742 CGGGAATTGCTTACGCGCCCGGCTCTCCGAAAGAGAGCTCTCCACCTTAGGC 683
QY 196 AGCTC 200
DB 682 TCCTC 678
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Job time: 212.322 secs





/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DF027YD08"  
/tissue\_type="FETAL BRAIN"  
/dev\_stage="fetal"  
/clone\_id="Homo sapiens FETAL BRAIN"  
/note="Organ: brain; Vector: PCWVSORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCWVSORT 6 vector. Library was not normalized."  
76 a 322 c 351 g 32 t 143 others

BASE COUNT  
ORIGIN  
Query Match 22.2%; Score 56; DB 13; Length 924;  
Best Local Similarity 41.2%; Pred. No. 0.14; Mismatches 92; Indels 0; Gaps 0;  
Matches 89; Conservative 35;

QY 14 GCGCGAGATGAGCTGATGCTGCGGCGCTCCCACTCCAGCGGAGAGGCGC 73  
DB 609 GCGCGGAGGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 668  
QY 74 CACGAGACCCCTGCTGCGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 133  
DB 669 GCGCGGAGGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 728  
QY 134 GCGCGAGATGAGCTGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 193  
DB 729 GCGCGGAGGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 788  
QY 194 GAAGCTCCCTCACCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 229  
DB 789 GCGCGGAGGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 824

RESULT 2  
BX425797 828 bp mRNA linear EST 15-MAY-2003  
LOCUS BX425797 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone  
DEFINITION CLOBB0302E01 3-PRIME, mRNA sequence.  
ACCESSION BX425797  
VERSION BX425797.1 GI:30784485  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 828)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Genoscope - Centre National de Sequencage  
Genoscope - 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 855c.f. For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CLOBB0302E01F1;cluster=855c.f. Contact :  
Feng Liang Email: fliang@life.techn.com URL: <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
Paradey Avenue Genoscope sequence ID : CLOBB0302E01F1.

FEATURES  
source  
1..828  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CLOBB0302E01"  
/tissue\_type="NEUROBLASTOMA"  
/clone\_id="Homo sapiens NEUROBLASTOMA"  
/note="Vector: PCWVSORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,

double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the PCWVSORT 6 vector.  
Library was not normalized."  
BASE COUNT 88 a 191 c 161 g 181 t 207 others  
ORIGIN

Query Match 22.1%; Score 55.8; DB 13; Length 828;  
Best Local Similarity 36.4%; Pred. No. 0.16; Mismatches 77; Indels 0; Gaps 0;  
Matches 72; Conservative 49;

QY 41 GCGCGCTCAGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 100  
DB 341 GCGCGCTCAGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 400  
QY 101 CCAGGCTGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 160  
DB 401 CCGMAAMVSS 460  
QY 161 GCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 220  
DB 461 CCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 520  
QY 221 GCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 238  
DB 521 GCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 538

RESULT 3  
BX384405/c 559 bp mRNA linear EST 08-MAY-2003  
LOCUS BX384405 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens  
DEFINITION CSD0K009Y1P19 3-PRIME, mRNA sequence.  
ACCESSION BX384405  
VERSION BX384405.1 GI:30460453  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 559)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Genoscope - Centre National de Sequencage  
Genoscope - 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10148.f. For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CSD0K009Y1P19;cluster=10148.f. Contact :  
Feng Liang Email: fliang@life.techn.com URL: <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
Paradey Avenue Genoscope sequence ID : CSD0K009Y1P1.

FEATURES  
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/mol\_type="mRNA"  
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/clone="CSD0K009Y1P19"  
/tissue\_type="HELA CELLS COT 25-NORMALIZED"  
/cell\_line="HELA"  
/clone\_id="Homo sapiens HELA CELLS COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoRV sites of the PCWVSORT 6 vector. Library was normalized."  
BASE COUNT 92 a 88 c 106 g 94 t 179 others  
ORIGIN

Query Match 21.8%; Score 55; DB 13; Length 559;  
Best Local Similarity 17.3%; Pred. No. 0.22;









[illegible][illegible]

QY 186 ACNNGAGGAGGAGCTCCCTCAGCCCGGCGGAGGCGGCGG 231  
Bx462440/c  
Db 295 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 340

## RESULT 15

LOCUS Bx462440 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA  
DEFINITION clone CS0DH002ZH23 3-PRIME, mRNA sequence.  
ACCESSION Bx462440.1 GI:31019574  
KEYWORDS EST.

VERSION Bx462440.1 GI:31019574  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1. (bases 1 to 1201)  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
TITLE Li, W.B., Gruber, C., Jessee, J. and Polyes, D.  
JOURNAL Full-length cDNA libraries and normalization  
COMMENT Unpublished

CONTACT: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 9865.f  
Contact: Feng Liang Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID: CS0DH002CD12NP1.  
Location/Qualifiers

## FEATURES

source

1. 1201  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DH002ZH23"  
/issue\_type="T CELLS (JURKAT CELL LINE)"  
/cell\_line="JURKAT CELL LINE"  
/clone\_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"  
/note="Vector: PCMVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."

BASE COUNT 225 a 332 c 293 g 245 t 106 others

Query Match 19.9%; Score 50.2; DB 13; Length 1201;  
Best Local Similarity 40.3%; Pred. No. 2;  
Matches 94; Conservative 35; Mismatches 104; Indels 0; Gaps 0;

QY 6 GGGAGGCGCGCGGAGTGGAGGCTGATGCTCCCTGCGCTCCACCTCCCGAGCGGAG 65  
Db 1198 GGTTGTCGCGCGCGGCGGCGGCGGCGGCTTCYGGGKTTTSCSYCCCTCCSTGGGKGGGGGATK 1139  
QY 66 AAGCGCGCCACGAGACCCCGCAGTGGCCGAGCTTGCCAGAGTCTGCGATCAGAGCAGAGG 125  
Db 1138 KXGSCCGCGCTGCGGCGGCTTTCAGAGGCGGCGCTCCCGCTGCGGCGGCGGCGGCGG 1079  
QY 126 ACCAGGAGGAGGAGGAGTGGCGCGCGCGCGCGCGCTGCGCGGCGGAGGAGGAGTCTC 185  
Db 1078 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1019  
QY 186 ACNNGAGGAGGAGTCCCTCAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 238  
Db 1018 SSSBKKGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 966

RESULT 16  
Bx425080/c  
LOCUS Bx425080 Homo sapiens PLACENTA Homo sapiens cDNA clone Cl0BA0092F07  
DEFINITION 3-PRIME, mRNA sequence.  
1165 bp mRNA linear EST 15-MAY-2003

ACCESSION Bx425080  
VERSION Bx425080.1 GI:30772433  
KEYWORDS Est.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1. (bases 1 to 1165)  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
TITLE Li, W.B., Gruber, C., Jessee, J. and Polyes, D.  
JOURNAL Full-length cDNA libraries and normalization  
COMMENT Unpublished

CONTACT: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10451.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=Cl0BA0092F07FPI&cluster=10451.f. Contact :  
Feng Liang Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID: Cl0BA0092F07FPI.  
Location/Qualifiers

## FEATURES

source

1. 1165  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="Cl0BA0092F07"  
/issue\_type="PLACENTA"  
/clone\_lib="Homo sapiens PLACENTA"  
/note="Vector: PCMVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."

BASE COUNT 270 a 69 c 221 g 273 t 332 others

Query Match 19.7%; Score 49.6; DB 13; Length 1165;  
Best Local Similarity 17.1%; Pred. No. 2.6; DB 13; Length 1165;  
Matches 35; Conservative 95; Mismatches 75; Indels 0; Gaps 0;

QY 7 GGGAGGCGCGCGGAGTGGAGGCTGATGCTCCCTGCGCGCTCCCGAGCGGAGGAG 66  
Db 614 SSSSSSSSSSSSSSSSSSSSSSCCTTTTSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 555  
QY 67 AGCGCGCCACGAGACCCCGAGTGGCCGAGCTTGCCAGCGTCTGGAGTCAAGAGGAGGA 126  
Db 554 SSSSSSSSSSSSSSSSSSSSSSBRTSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 495  
QY 127 CAGAGGAGGAGGAGTGGCGCGCGCGCGCGCGCTGCGCGGCGGAGGAGGAGTCTC 186  
Db 494 CCG 435  
QY 187 CCGAGGAGGAGTCCCTCAGCCCGG 211  
Db 434 SSSSBKKGKKTTCCTCCCGCGG 410

RESULT 17  
CNS0200G  
LOCUS CNS0200G  
DEFINITION Tetradodon nigroviridis genome survey sequence T7 end of clone  
15806 of library G from Tetradodon nigroviridis, genomic survey  
sequence.  
ACCESSION AL209545.1 GI:7868364  
VERSION AL209545.1  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetradodon nigroviridis  
ORGANISM Tetradodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;



[illegible]

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (Bases 1 to 1169)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL  
 COMMENT Unpublished  
 Contact: Robert Strussberg, Ph.D.  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
 Plate: LAM12769 row: 1 column: 01  
 High quality sequence stop: 334.  
 Location/Qualifiers  
 1. 1169  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5745864"  
 /tissue\_type="leukocyte"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH MGC 118"  
 /note="Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV  
 (destroyed); RNA source: leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library."  
 BASE COUNT 78 a 391 c 585 g 65 t 50 others  
 ORIGIN  
 Query Match 19.5%; Score 49.2; DB 12; Length 1169;  
 Best Local Similarity 49.0%; Pred.No. 3.1; Mismatches 128; Indels 0; Gaps 0  
 Matches 123; Conservative  
 Oy 2 GGCCTGGGAGCGCGCCGGAGTGAAGCCCTGATCTCTCTTGCGCCCTTCACCTTCCCGAGC 61  
 Db 595 GGG 654  
 Oy 62 GCAGAAAGCGCCACAGAGAGACCCCAAGTCCCGACGTTGACAGCGTCTGGAGTACAGAGC 121  
 Db 655 GCGGG 714  
 Oy 122 AGGAGCAGAGAGCCAGAGAACTGCGCGCGCCCGCCCTTCGCTTGCGCGAGGAGAGCTC 181  
 Db 715 GAGCC 774  
 Oy 182 CCTCAGCAGAGAGAGAGTCTCCCTCAACCGCGCCAGCGCCTTGACAGGGGGGCGGTGGAGTCA 241  
 Db 775 CCGGCGCGCGGGCC 834  
 Oy 242 GACCGCAAGC 252  
 Db 835 GCAGGGGCGGCG 845

REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 TITLE 1 (bases 1 to 935)  
 AUTHORS Genoscope.  
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
 Web : www.genoscope.cns.fr)

## COMMENT

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs for further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ohsogawa and Aaron Mammoser in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pi and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

## source

1..935  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"  
 /clone\_lib="RPCI-98"  
 /note="end : T7"  
 Location/Qualifiers  
 BASE COUNT 257 a 170 c 162 g 96 t 250 others  
 ORIGIN

Query Match 19.4%; Score 49; DB 29; Length 935;  
 Best Local Similarity 31.7%; Pred. No. 3.3; Mismatches 99; Indels 0; Gaps 0;  
 Matches 73; Conservative 58; Mismatches 99; Indels 0; Gaps 0;

QY 3 GCGGGGAGGCGCGGAGTGAAGCTTATGTCCTTGGCGCCCTCCACCTCCAGGCG 62  
 DB 694 GCGGGGAGGCGCGGAGTGAAGCTTATGTCCTTGGCGCCCTCCACCTCCAGGCG 753  
 QY 63 CAGAAGCGCCCAAGAGACCCCACTGCTCCCACTGCTCCCACTGCTCCCACTGCTCC 122  
 DB 754 CCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 813  
 QY 123 GGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 182  
 DB 814 GCGGGGAGGCGCGGAGTGAAGCTTATGTCCTTGGCGCCCTCCACCTCCAGGCG 873  
 QY 183 CTCACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 232  
 DB 874 GCGGGGAGGCGCGGAGTGAAGCTTATGTCCTTGGCGCCCTCCACCTCCAGGCG 923

RESULT 20  
 CENS015Y4/c 1203 bp DNA linear GSS 26-JUL-1999  
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC  
 DEFINITION BACN15E10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 AL106054  
 AL106054.1 GI:5619805  
 GSS.  
 Drosophila melanogaster (fruit fly)  
 SOURCE Drosophila melanogaster  
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 REFERENCE 1 (bases 1 to 1203)  
 AUTHORS Genoscope.  
 TITLE Direct Submission

JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
 Web : www.genoscope.cns.fr)  
 Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (DrosBAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Rayan. It has been constructed in the vector peloBAC11.

## COMMENT

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs for further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ohsogawa and Aaron Mammoser in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pi and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

## source

1..1203  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"  
 /clone\_lib="DrosBAC"  
 /plasmid="peloBAC11"  
 /note="end : T7"  
 Location/Qualifiers  
 BASE COUNT 154 a 274 c 380 g 158 t 237 others  
 ORIGIN

Query Match 19.4%; Score 49; DB 29; Length 1203;  
 Best Local Similarity 36.1%; Pred. No. 3.3; Mismatches 108; Indels 0; Gaps 0;  
 Matches 87; Conservative 46; Mismatches 108; Indels 0; Gaps 0;

QY 7 GGGAGGCGCGGAGTGAAGCTTATGTCCTTGGCGCCCTCCACCTCCAGGCGCAGA 66  
 DB 1196 GGGAGGCGCGGAGTGAAGCTTATGTCCTTGGCGCCCTCCACCTCCAGGCGCAGA 1137  
 QY 67 AGGCGCCACAG 126  
 DB 1136 GGGAGGCGCGGAGTGAAGCTTATGTCCTTGGCGCCCTCCACCTCCAGGCGCAGA 1077  
 QY 127 CAGAAGCGCCCAAGAGACCCCACTGCTCCCACTGCTCCCACTGCTCCCACTGCTCC 186  
 DB 1076 GGGAGGCGCGGAGTGAAGCTTATGTCCTTGGCGCCCTCCACCTCCAGGCGCAGA 1017  
 QY 187 CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 246  
 DB 1016 GCGGGGAGGCGCGGAGTGAAGCTTATGTCCTTGGCGCCCTCCACCTCCAGGCG 957  
 QY 247 C 247  
 DB 956 C 956

RESULT 21  
 CENS0072Q/c 932 bp DNA linear GSS 03-JUN-1999  
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #  
 DEFINITION BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 AL066742  
 AL066742.1 GI:4945205  
 GSS.  
 Drosophila melanogaster (fruit fly)  
 SOURCE Drosophila melanogaster  
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 932)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
 Web : www.genoscope.cns.fr)  
 Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (DrosBAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Rayan. It has been constructed in the vector peloBAC11.

melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source

1. 932  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone\_lib="RPCL-98"  
/note="end : 17"

BASE COUNT 155 a 202 c 241 g 91 t 243 others  
ORIGIN

Query Match 19.4%; Score 48.8; DB 29; Length 932;  
Best Local Similarity 35.0%; Pred. No. 3.6;  
Matches 90; Conservative 62; Mismatches 100; Indels 5; Gaps 1;

QY 1 CGGCGGAGGCGCGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCCGAG 60  
DB 715 CGGSCGSGCGCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 656  
QY 61 CGCAGAGGCGCGCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 120  
DB 655 GCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 596  
QY 121 CAGGAGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 175  
DB 595 CAVARAAVSVCCCGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 536  
QY 176 AAGCTCCCTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 235  
DB 535 CAGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 476  
QY 236 GCGTCGAGCGCGGAGG 252  
DB 475 CGVAGGCGCGGCGGCGG 459

RESULT 22  
AG074680/c 986 bp DNA linear GSS 03-NOV-2001  
LOCUS AG074680  
DEFINITION Pan troglodytes DNA, clone: PTB-066N16.R, genomic survey sequence.  
ACCESSION AG074680  
VERSION AG074680.1 GI:16626482  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
REFERENCE  
AUTHORS Fukuyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
TITLE BAC end sequences of library PTB  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 986)  
Fukuyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
TITLE BAC end sequences of library PTB  
JOURNAL Unpublished

REFERENCE  
AUTHORS Fukuyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
TITLE BAC end sequences of library PTB  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 986)  
Fukuyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
TITLE BAC end sequences of library PTB  
JOURNAL Unpublished  
SUBMITTED (02-AUG-2001) Asao Fukuyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan  
1-7-22 Suhei-ro-chou, Tsukuba, Ibaraki, 305-8565, Japan  
(E-mail: [chimpsgsc@riken.go.jp](mailto:chimpsgsc@riken.go.jp), URL: <http://hgp-gsc.riken.go.jp/>,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB. This BAC and  
COMMENT was generated during the R&D process and may have higher chance of

clone tracking errors.

## PRIMERS

Sequencing: M13rev  
LIBRARY

Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI  
Location/Qualifiers

## FEATURES

source

1. 986  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone\_lib="PTB-066N16.R"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC library"  
/note="end : 17"

BASE COUNT 15 a 433 c 495 g 10 t 33 others  
ORIGIN

Query Match 19.4%; Score 48.8; DB 29; Length 986;  
Best Local Similarity 50.2%; Pred. No. 3.6;  
Matches 116; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 2 GCGCGGAGGCGCGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCCGAG 61  
DB 414 GCGGCGGCGCGCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 355  
QY 62 GCAGAGGCGCGCGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCG 121  
DB 354 GCGGCGGCGCGCGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCG 295  
QY 122 AGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 181  
DB 294 CCGGCGGCGCGCGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCG 235  
QY 182 CCGGCGGCGCGCGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCG 232  
DB 234 CCGGCGGCGCGCGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCG 184

RESULT 23  
B0712096/c 902 bp RNA linear EST 16-JUN-2002  
LOCUS B0712096  
DEFINITION AGENCOURT\_8351502 NIH\_MGC\_113 Homo sapiens CDNA clone IMAGE:6282461  
ACCESSION B0712096  
VERSION B0712096.1 GI:21850995  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs@remail.nih.gov](mailto:cgabs@remail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LCCM2476 row: 0 column: 06  
High quality sequence start: 4  
Location/Qualifiers

## FEATURES

source

1. 902  
/organism="Homo sapiens"  
/mol\_type="RNA"  
/db\_xref="taxon:9606"

/clone="IMAGE:6282461"  
/lab host="DH10B (phage-resistant)"  
/clone.lib="NIH\_MGC.lib"  
/note="Organism: E.coli; Vector: pOTM7; Site 1: XhoI; Site 2:  
EcoRI; CDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GCGACGAG(G) library constructed by Ling Hong in the  
Laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and  
SuperScript II RT (Life Technologies). Note: this is a  
NIH\_MGC library."  
BASE COUNT 85 a 403 c 271 g 123 t 20 others  
ORIGIN

Query Match 19.3%; Score 48.6; DB 13; Length 902;  
Best Local Similarity 49.4%; Pred. No. 4;  
Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 5 CGGGAGAGCGCGCGGAGTGAAGCCCTGATGTCCTGCGCGCTTCCACCTCCAGCCCA 64  
DB 793 CGGAGAGGCGCGCGCGGAGAGGCGCCAGAGACCCCGCGCGCGCGCGCGCGG 734  
QY 65 GAAGCG 124  
DB 733 GAAGCG 674  
QY 125 GACGAGGAGCG 184  
DB 673 GCG 614  
QY 185 CACGCGAGGAGCG 235  
DB 613 GGGGCG 563

## RESULT 24

EX391246 1061 bp mRNA linear EST 13-MAY-2003  
LOCUS EX391246 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
DEFINITION clone:CS0D10081N19.3-PRIME, mRNA sequence.  
ACCESSION EX391246  
VERSION EX391246.1 GI:30615383  
KEYWORDS EST.

## SOURCE

ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1061)  
L.I.W.B., Gruber, C., Jesses, J. and Polayes, D.  
Full-length CDNA libraries and normalization  
Unpublished

## REFERENCE

AUTHORS BP 191 91006 EVRY cedex - France  
TITLE Email: segre@genoscope.cns.fr; Web: www.genoscope.cns.fr  
JOURNAL Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 7394.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0BAH012ZH06P1&cluster=7394.f. Contact :  
Feng Liang Email: fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0BAH012ZH06NP1.  
Location/Qualifiers  
1. 1061

## FEATURES

source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS0D10081N19"  
/issue\_type="PLACENTA COT 25-NORMALIZED"  
/note="1st strand CDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand CDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 225 a 153 c 229 g 289 t 165 others  
ORIGIN

Query Match 19.3%; Score 48.6; DB 13; Length 1061;  
Best Local Similarity 29.9%; Pred. No. 4;  
Matches 64; Conservative 62; Mismatches 88; Indels 0; Gaps 0;

QY 1 CGCGCGGAGAGCGCGCGGAGTGAAGCCCTGATGTCCTGCGCGCTTCCACCTCCAG 60  
DB 584 CGCGCGGAGAGCGCGCGGAGTGAAGCCCTGATGTCCTGCGCGCTTCCACCTCCAG 525  
QY 61 CGCAGAGGCG 120  
DB 524 CCG 465  
QY 121 CAGGAGCAGGAGCG 180  
DB 464 SSSCGSS 405  
QY 181 CCTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 214  
DB 404 CCG 371

## RESULT 25

AL514261 1201 bp mRNA linear EST 08-MAY-2003  
LOCUS AL514261 Homo sapiens NEUROBLASTOMA Homo sapiens CDNA clone  
DEFINITION clone:BB007ZG11.3-PRIME, mRNA sequence.  
ACCESSION AL514261  
VERSION AL514261.2 GI:30464146  
KEYWORDS EST.

## SOURCE

ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1201)  
L.I.W.B., Gruber, C., Jesses, J. and Polayes, D.  
Full-length CDNA libraries and normalization  
Unpublished

## REFERENCE

AUTHORS BP 191 91006 EVRY cedex - France  
TITLE Email: segre@genoscope.cns.fr; Web: www.genoscope.cns.fr  
JOURNAL Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 9246.r For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CL0BB007ZG11P1&cluster=9246.r. Contact :  
Feng Liang Email: fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CL0BB007ZG11P1.  
Location/Qualifiers  
1. 1201

## FEATURES

source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CL0BB007ZG11"  
/issue\_type="NEUROBLASTOMA"  
/note="Vector: pCMVSPORT 6; 1st strand CDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand CDNA was digested with Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was not normalized."  
BASE COUNT 161 a 217 c 183 g 354 t 286 others  
ORIGIN

Query Match 19.3%; Score 48.6; DB 9; Length 1201;  
Best Local Similarity 40.4%; Pred. No. 4;

Matches 92; Conservative 33; Mismatches 103; Indels 0; Gaps 0;

QY 4 CCGGAGAGCGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCG 63  
 Db 369 CCGGAGAGCGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCG 421  
 QY 64 ACAAGAGCGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCG 123  
 Db 422 GCG 481  
 QY 124 GAGACGAGAGCGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCG 183  
 Db 482 VAAAGAGAGCGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCG 541  
 QY 184 TCACGAGAGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCG 231  
 Db 542 CCGCGAGAGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCG 589

RESULT 26  
 AL514267 1172 bp mRNA linear EST 08-MAY-2003  
 LOCUS AL514267 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone  
 DEFINITION AL514267 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone  
 ACCESSION AL514267  
 VERSION AL514267  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 1172)  
 Li W.B., Gruber C., Jesse J., and Polayes D.  
 Full-length cDNA libraries and normalization  
 Unpublished  
 On Feb 13 2001 this sequence version replaced gi:12777761.  
 Contact: Genoscope  
 Genoscope Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seque@genoscope.cns.fr; Web: www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 6437.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=AL514267&cluster=6437.r. Contact :  
 Feng Liang Email: fliang@life.technet.com URL :  
 http://fulllength.invitrogen.com/ invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CL08B007ZD09FPI.  
 Location/Qualifiers  
 1. 1172  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CL08B007ZD09"  
 /tissue\_type="NEUROBLASTOMA"  
 /clone\_lib="Homo sapiens NEUROBLASTOMA"  
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
 with a NotI-oligo(dT) primer. Five prime end enriched  
 double-strand cDNA was digested with Not I and cloned into  
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
 Library was not normalized."  
 BASE COUNT 35 a 476 c 244 g 241 t 176 others  
 ORIGIN

Query Match 19.2%; Score 48.4; DB 9; Length 1172;  
 Best Local Similarity 41.9%; Pred. No. 4.4;  
 Matches 90; Conservative 28; Mismatches 97; Indels 0; Gaps 0;

QY 13 CCGCGGAGAGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCGCG 72  
 Db 311 YBCCGCGGAGAGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCGCG 370  
 QY 73 CCGCGGAGAGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCGCG 132

Db 371 CCGCGGAGAGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCGCG 430  
 QY 133 AGCGAGAGAGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCGCG 192  
 Db 431 GCGCGGAGAGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCGCG 490  
 QY 193 GGAAGCGGAGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCGCG 227  
 Db 491 GCGCGGAGAGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCGCG 525

RESULT 27  
 A2189053 845 bp DNA linear GSS 30-AUG-2000  
 LOCUS A2189053  
 DEFINITION Sp\_1013\_B1\_B04\_Spec Strongylocentrotus purpuratus, purple sea  
 urchin, sperm genomic BAC library Strongylocentrotus purpuratus  
 genomic clone Plate=1013 Col=7 Row=D, genomic survey sequence.  
 A2189053 GI:8372232  
 GSS.  
 ACCESSION Strongylocentrotus purpuratus  
 VERSION Strongylocentrotus purpuratus  
 KEYWORDS Strongylocentrotus purpuratus  
 ORGANISM Strongylocentrotus purpuratus  
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 Echinoidea; Euechinoidea; Echinacea; Echinoida;  
 Strongylocentrotidae; Strongylocentrotus.  
 1 (bases 1 to 845)  
 Cameron, R.A., Mahliras, G., Rast, J.P., Martinez, P., Biondi, T.R.,  
 Swartzell, S., Wallace, J.C., Poultke, A.J., Livingston, B.T., Wray  
 G.A., Etensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and  
 Hood, L.  
 A sea urchin genome project: Sequence scan, virtual map, and  
 additional resources  
 Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)  
 20402566  
 PUBMED 10920195  
 Contact: Cameron, RA, Davidson, EH, Hood, L  
 Division of Biology 156-29  
 California Institute of Technology  
 Pasadena California 91125, USA  
 Tel: (626) 395-8421  
 Fax: (626) 793-3047  
 Email: acameron@caltech.edu  
 Plate: 1013 row: D column: 7  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 845.  
 Location/Qualifiers  
 1. 845  
 /organism="Strongylocentrotus purpuratus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7668"  
 /clone="Plate=1013 Col=7 Row=D"  
 /clone\_lib="Strongylocentrotus purpuratus, purple sea  
 urchin, sperm genomic BAC library"  
 /note="Organ: sperm; Vector: BACs 6; BAC Clones in E-Coli  
 DH10B"  
 BASE COUNT 30 a 368 c 300 g 117 t 30 others  
 ORIGIN

Query Match 19.1%; Score 48.2; DB 28; Length 845;  
 Best Local Similarity 48.2%; Pred. No. 4.8;  
 Matches 119; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 1 CCGCGGAGAGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCG 60  
 Db 294 CCGCGGAGAGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCGCG 353  
 QY 61 CCGAGAGAGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCGCG 120  
 Db 354 CCGCGGAGAGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGCGCG 413  
 QY 121 CAGGAGAGAGCGGAGTGAAGCTGTCCTGCGCGCTCCACCTCCAGAGGAGT 180

Db	414	CGGNGGCGCGAGNTCCCCGGCCCCCCCCCGGCGCCCGCGCGCGCGCGCGTGGCGGGC	473
QY	181	CCCTCACNMGAGGAAGCTCCCTCAACCGGGCCAGCCTGTACAGGGGAGCGCGTGATTC	240
Db	474	CGGCGCGGCGCGCGGGGCGGCGTCCCCCGCGGCGGGGCGCGGGGGGCGNGACT	533
QY	241	AGACCGC 247	
Db	534	CCGCGGC 540	

RESULT	28
CNS006X/c	
LOCUS	
DEFINITION	CNS006X Drosophila melanogaster genome survey sequence T7 end of BAC # BACH1409 of RPc1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL066051
VERSION	AL066051.1 GI:4945019
KEYWORDS	GSS.
SOURCE	Drosophila melanogaster (fruit fly)
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Epiphytoidae; Drosophilidae; Drosophila. 1 (bases 1 to 935) Genoscope. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	

COMMENT

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see [http://www.fruitfly.org/The\\_BDGP/drosophila\\_melanogaster\\_BAC\\_library](http://www.fruitfly.org/The_BDGP/drosophila_melanogaster_BAC_library) was prepared by Kazunoyo Oosagawa and Aaron Mammone in Pierlet de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain *YZ, cn bw sp*, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES	
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1..935	
/organism="Drosophila melanogaster"	
/mol_type="genomic DNA"	
/db_xref="taxon:7227"	
/clone="BACR14N09"	
/clone_1fb="RPC1-98"	
/note="end : 17"	
257 a	170 c 162 g 96 t 250 others
BASE COUNT	
BRIGIN	

[illegible]

LOCUS	DEFINITION	1201 bp	mRNA	linear	EST 13-May-2003
LOCUS	BX422338				
DEFINITION	BX422338 Homo sapiens FETAL LIVER Homo sapiens CDNA clone				
ACCESSION	BX422338				
VERSION	BX422338.1	GI:30659284			

REFERENCE	1. (bases 1 to 1201)
AUTHORS	Li, W. B., Gruber, C., Jesssee, J. and Polayee, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
COMMENT	Contact: Genoscope

**FEATURES**  
**source**  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 6006.r For  
 more information about this cluster, see  
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSD0M003DF020PL&cluster=6006.r)  
 cgi-bin/cluster.cgi?seq=CSD0M003DF020PL&cluster=6006.r. Contact :  
 Feng Liang Email : fliang@life tech.com URL :  
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CSD0M003DF020PL.  
 Location/Qualifiers  
 1..1201

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/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="CS0DM003yL04"
/rnause_type="FETAL LIVER"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/notes="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-Oligo(dT) primer. Five prime end
was enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalised."
BASE COUNT      251 a      334 c      358 g      111 t      147 others
ORIGIN

```

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT
BX415926/c	BX415926	1144 bp	mRNA	linear	EST 13-MAY-2003				
LOCUS	BX415926	1144 bp	mRNA	linear	EST 13-MAY-2003				
DEFINITION	BX415926 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008YH01								
ACCESSION	BX415926								
VERSION	BX415926								
KEYWORDS	5-PRIME, mRNA sequence.								
ORGANISM	BX415926.1 GI:30650131								
REFERENCE	EST.								
AUTHORS	Homo sapiens (human)								
TITLE	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
JOURNAL	1 Dbases 1 to 1144								
COMMENT	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished								
FEATURES	Contact: Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France								
SOURCE	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to technology cluster 9016.f For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0CAP008CD01Q1P1&cluster=9016.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0CAP008CD01Q1P1.								
BASE COUNT	230 a 297 c 389 g 123 t 105 others								
ORIGIN	1..1144								
	/organism="Homo sapiens"								
	/mol_type="mRNA"								
	/db_xref="taxon:9606"								
	/clone="CS0CAP008YH01"								
	/tissue_type="THYMUS"								
	/clone_id="Homo sapiens THYMUS"								
	/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."								
Query Match	18.9%; Score 47.6; DB 13; Length 1144;								
Best Local Similarity	38.3%; Pred. No. 6.3;								
Matches	80; Conservative 37; Mismatches 92; Indels 0; Gaps 0;								
QY	11 GCCGCGCCGAGTGCAGGCGCTTATCTGCTCCCTGCGCCTTCCACCTTCCCGCAGGCGCAGAAAGC 70								
DB	1006 GSGGSGSSGGCGSGSGSGSSGSGSGSGSGSGSSCCCGSGSGSGCGGCGGSGCGSG 947								
QY	71 GCCCAGCAGGAGACCCCACTGCGCCGACGCTTGCCACCGTGTGGATACAGAGGAGACCGAG 130								
DB	946 GSGCGCGSGGGGGCCCCCGGGGCGCGCCCCCGSGCGCCCGGCGGGCGCCGCCGCCGCC 887								
QY	131 GGAGCCAGAACTGCGCGCGCCCGCCCGCTGCGCTGCGGCGCAGGAGAACTGCTTACACNG 190								
DB	886 SGGCGCGCGGSGCGCGCCSGGCGCCSGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 827								
QY	191 AGGAGAGTCCCTTACACCGCGCGCCGCCGCC 219								
DB	826 GGSAGSCCCCCCGGCGSSGCCCCCGCCCC 798								
RESULT 31	CNS016E3	1201 bp	DNA	linear	GSS 26-JUL-1999				
LOCUS	CNS016E3								
DEFINITION	Drosophila melanogaster genome survey sequence 17 end of BAC								
	BAC1315 of Drosophila library from Drosophila melanogaster (fruit								
	fly), genomic survey sequence.								
ACCESSION	AL106629								
VERSION	AL106629.1								
KEYWORDS	GI:5622856								

SOURCE	ORGANISM
Drosophila melanogaster (fruit fly)	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 1201)  Genoscope, Direct Submission Submitted (23-JUL-1998) Genoscope - Centre National de Sequençage : BP 10610 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (/dwdsg.bnl.ac.uk) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector peloBAC11.
FEATURES	Location/Qualifiers
source	1..1201 organism="Drosophila melanogaster" mol_type="genomic DNA" db_xref="taxon:7227" clone="BACN15A15" clone_1lb="DroSBAC" plasmid="peleOBAC11" note="end : T7"
BASE COUNT	211 a        300 c        350 g        168 t        172 others
ORIGIN	
Query Match	18.9% Score 47.6; DB 29; Length 1201;
Best Local Similarity	43.6%; Pred. No. 6.3; Mismatches 68; Indels 0; Gaps 0;
Matches	72; Conservative 25; Mismatches 68; Indels 0; Gaps 0;
OY	82 CCCCAGTGGCCGCGCTTGCAAGGTGTGCATCAGAAGCACGAAGACCACAGAA 141
DB	916 CCCGCCGSSSGGGGGGGGGGGGGGGGNKCCCCCSCGGGGGGSSGGGGGGGGG 975
OY	142 CTGGCGCCGCCCGCCCTTCGTGCTGGCGCGACAAGACTCCCTACCNAGAGAACCTCC 201
DB	976 GGSSCSGCCCCCCCCCCCCNCNGCGCGAGSCSAAMMACMSSSVMAAGGS GCCC 1035
OY	202 CCTCACCCGCGCCACCTGCAGAGGGGGCGCGTGGGGGTCAAGCCG 246
DB	1036 CCCCCSSCCCCCGCCCGSSGGGGGGGRRARRRARRRVG 1080
RESULT 32	
CNS043G6	384 bp DNA linear GSS 01-SEP-2000
TETRADON NIGROVIRIDIS genome survey sequence pUC-Ori end of clone	
DEFINITION	079J07 of library G from Tetradodon nigroviridis, genomic survey sequence.
VERSION	AL272751 GI:7994989
KEYWORDS	GSS: genome survey sequence.
SOURCE	Tetradodon nigroviridis Tetradodon nigroviridis Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Rutelosteoi; Neoteleostei; Acanthomormphi; Acanthopterygii; Perciformes; Tetraodontifomes; Tetraodontoidae; Tetraodontidae; Tetradodon.
REFERENCE	Roeck Croillon,H., Jailion,O., Dasilva,C., Bouneau,L., Fisher.C., Benou,A., Fitznes,C., Wincker,P., Brocletier,F., Queller.F., Saunier,W. and Weissenbach,J. Estimate of human gene number provided by genome-wide analysis using Tetradodon nigroviridis DNA Sequence. Journal Nat. genet. 25 (2), 235-238 (2000).
JOURNAL MEDLINE PUBMED REFERENCE	20296633 10835645







BASE COUNT 213 a 377 c 395 g 162 t 88 others

Query Match 18.8%; Score 47.4; DB 12; Length 1235;  
Best Local Similarity 47.6%; Pred. No. 6.9;  
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

11 GGGGGGCGGAGAGTGAAGCTGATCGTCTGCGGCTCTCCACCTCCCGAGCGCAGAAAGGC 70  
940 GGGGAGCTCCCGGGGCGCCCGGGGGGCGCCGAGGCGCGCCCGGGGGGCGCGCGCGC 999  
71 GCGCCAGAGAGAGCCCGCAGTGCAGGTCGCCAGGTCGTGGATCAGAGGAGGAGCAG 130  
1000 CCCCCCGGGCCCGCCCGCCCGCCCAACGCGCGCGCGCGCGCGCGCGCGCGCGCG 1059  
131 GAGGCGAGAGACTGCG 190  
1060 CGCGGCGGGGGGCG 1119  
191 AGGGAAGCTCTCCCTCAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 237  
1120 NGGAGGCG 1166

RESULT 37 924 bp mRNA linear EST 15-MAY-2003  
BX442207 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
LOCUS BX442207  
DEFINITION CS0DF027YD08 5-PRIME, mRNA sequence.

ACCESSION BX442207  
VERSION BX442207  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 924)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of Invitrogen Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Paraday Avenue Genoscope sequence ID: CS0DF027YD04Qp1.

FEATURES  
source

1. 924  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DF027YD08"  
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/dev\_stage="fetal"  
/clone\_lib="Homo sapiens FETAL BRAIN"  
/note="Organ: brain; Vector: pCMVSPORT\_6; 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."  
BASE COUNT 76 a 322 c 351 g 32 t 143 others

Query Match 18.7%; Score 47.2; DB 13; Length 924;  
Best Local Similarity 38.6%; Pred. No. 7.5;  
Matches 91; Conservative 35; Mismatches 110; Indels 0; Gaps 0;

1 CGCGCGGAGAGGCGGAGTGAAGCTGATCGTCTGCGGCTCTCCACCTCCCGAGG 60  
827 CGCGCGGAGAGGCGGAGTGAAGCTGATCGTCTGCGGCTCTCCACCTCCCGAGG 768

61 CGCAGAGGCGCCCGCAGAGAGCCCGCAGTCCCGCAGCTTGCCAGGATCAGAG 120  
767 CGGAGGCGGCGCCCGCAGAGAGCCCGCAGTCCCGCAGGATCAGAG 708  
121 CAGGAGACGAGAGAGCGAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
707 SSCCGCGCGGCG 648  
181 CCTTACCGGAGAGAGTCTCCCTCAGCCCGCGCGCGCGCGCGCGCGCGCGCG 236  
647 CCG 592

RESULT 38 976 bp DNA linear GSS 26-JUL-1999  
CNS010DY/c  
LOCUS CNS010DY/c  
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC BACN03N21 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL098845.1 GI:5610456  
VERSION AL098845  
KEYWORDS GSS.  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster (fruit fly)  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 976)  
Genoscope.  
Direct Submission  
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage; BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)  
- Web: www.genoscope.cns.fr  
determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Bros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

COMMENT

FEATURES  
source

1. 976  
/organism="Drosophila melanogaster"  
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/note="end: 576"  
BASE COUNT 199 a 151 c 170 g 190 t 266 others

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Best Local Similarity 33.3%; Pred. No. 7.5;  
Matches 78; Conservative 45; Mismatches 111; Indels 0; Gaps 0;

4 CGCGGAGGCGGCGGAGTGAAGCTGATCGTCTGCGGCTCTCCACCTCCCGAGGCG 63  
546 SCSSSSSSSCNCCCGGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 487  
64 AGAAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 123  
486 CGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 427  
124 GAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 183  
426 AGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 367  
184 TCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 237  
366 SAVAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 313

RESULT	39
LOCUS	BX380510
DEFINITION	BX380510 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0D1054YE15 5-PRIME, mRNA sequence.
ACCESSION	BX380510
VERSION	BX380510.1 GI:30448885
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 994) Li, W.B., Gruber, C., Jessee, J., and Polayes, D. Full-length cDNA libraries and normalization Unpublished Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seqe@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/InvitrogenCorporation.1600 Paradise Avenue Genoscope sequence ID : CS0D1054AC08Qp1.
FEATURES	location/Qualifiers 1..994 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0D1054YE15" /libsize_type="PLACENTA COT 25-NORMALIZED" /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="Left strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT	273 a 200 c 211 g 139 t 171 others
ORIGIN	
Query Match	18.7%; Score 47.2; DB 13; Length 994;
Best Local Similarity	37.1%; Pred. No. 7.5; Indels 0; Gaps 0;
Matches	85; Conservative 41; Mismatches 103;
Db	4 CGGGGAGGCGGCGGAGTAGAGGCTATGTCCTCGGCGGCTCCACACTGCCGAGGCG 63
OY	380 CCCCVVRRRRRRRRRRRRRRGRGAGGGGGGSGSCSCCCCCCCCCCCCCCCC 439
Dd	64 AGAAGGCGCCCAAGAGACCCTCATGCTCCACGTTTGACAGGTCTGGATTAGAGCAG 123
OY	440 CSHCCCCCCCCCAAACCCCCCCCCMMTCSSCCCTCTCTAAACGAGKGGISTTCCCCC 499
Dd	124 GAACCAAGAGCTCAGAAGCTGCAGCGCGCCCGCCCGCTGCTCTGAGCGGAGGAAGTCC 183
OY	500 CCTMAAGGCCCCCCCTYSTGGGGGYCCCCCYCCCCCCCCCGGAGGTAMCCCCCTCT 559
Dd	184 TCACCGNAGAGGAAGCTCCCTCAGACCCGCGCCAGCCCTGAGGAGGGAGCGC 232
OY	560 CCCCCCTAASCCCTCTCTCTCYGAGKGGSSTCCCTCMTARAGGAGGGSYSY 608
RESULT	40
LOCUS	BX407619
DEFINITION	BX407619 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DB005Y1111 5-PRIME, mRNA sequence.
ACCESSION	BX407619
VERSION	BX407619.1 GI:30762809
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1000 bp mRNA linear EST 15-MAY-2000

1 (bases 1 to 1000)  
 Li, M. B., Gruber, C., Jessee, J. and Polayres, D.  
 Full-length cDNA libraries and normalization  
 Unpublished  
 COMMENT  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 Bp 191 91006 Evry cedex - France  
 Email: seqre@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by life technologies, a division of  
 invitrogen. This sequence belongs to sequence cluster 6789.f For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0AS0052D02Q1c&cluster=6789.f. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0AS0052D02Q1.  
 location/Qualifiers  
 1. 1000  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DE005Y119"  
 /issue\_type="PLACENTA"  
 /clone\_lib="Homo sapiens PLACENTA"  
 /note="Vector: PCWMSPORT 6; 1st strand cDNA was primed  
 with a NotI-oligo(dT) primer. Five prime end enriched,  
 double-strand cDNA was digested with Not I and cloned into  
 the Not I and EcoRV sites of the PCWMSPORT 6 vector.  
 Library was not normalized."  
 BASE COUNT 226 a 205 c 283 g 57 t 229 others  
 ORIGIN  
 Query Match 19.7%; Score 47.2; DB 13; Length 1000;  
 Best Local Similarity 21.1%; Pred. No. 7.5;  
 Matches 50; Conservative 95; Mismatches 92; Indels 0; Gaps 0;  
 Oy 2 GGGCGGGAGGCGGCGGGAGTGAAGCCTTGATGCTTCCTCGGCGCTCCACCTCCCGAGC 61  
 Db 443 GVCSSGGGGGGGGGGGGGCVAAAGGGGGCCSGGGGGGGGGGGGGGGGARRSSGGSCSG 502  
 Oy 62 GCAGAAAGCGCCACGAGAGACCCCACTGCGCCGACGTTGCCACGATGTGGANTAGAGGC 121  
 Db 503 SCCSSGGGGGGCGTCWCGSGGGGGCGSSSSGAGSSSGSGSGSSSSSSSSSSSSSSSV 562  
 Oy 122 AGGAGACCGAGGAGCAGAACTGCGCGCGCCCGCCCGCTCGGCGCCGAGGAGAGCTC 181  
 Db 563 AVSSSVSSSSSSSSSSSRASSSSSSSVVVVAAVAVSSGSGSSGAAAGGGS 622  
 Oy 182 CCTCAACGAGAGGAGACTCCCTCAACCGCGGACCGCTCGAGGGGGCGCGTGAGG 238  
 Db 623 SSGSSSSSSSSSSSSSSSGSSSSSGSSSSSGGGGGSVSGSSSAGCGGGCGGCGR 679

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 06:13:41; Search time 1957.81 Seconds

(without alignments)  
6749.284 Million cell updates/sec

Title: US-10-081-817a-19\_COPY\_229\_551

Perfect score: 323

Sequence: 1 gcgcgtggtgagccgca.....gcgccgagcccgccgc 323

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

GenEmbl:  
1: gb\_da:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_ma:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hcg\_hum:\*  
31: em\_hcg\_inv:\*  
32: em\_hcg\_other:\*  
33: em\_hcg\_mus:\*  
34: em\_hcg\_pln:\*  
35: em\_hcg\_rod:\*  
36: em\_hcg\_mam:\*  
37: em\_hcg\_vrt:\*  
38: em\_ey:\*  
39: em\_hugo\_hum:\*  
40: em\_hugo\_mus:\*  
41: em\_hugo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysts of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match	Length	DB	ID	Description
C 1	312	96.6	127488	2	AC022095	AC022095 Homo sapi
C 2	312	96.6	168347	2	AC025336	AC025336 Homo sapi
C 3	312	96.6	190024	9	AC122714	AC122714 Homo sapi
C 4	304.8	94.4	130129	2	AC108083	AC108083 Homo sapi
5	301	93.2	166777	2	AC106813	AC106813 Homo sapi
6	120	37.2	166777	2	BD082141	BD082141 Reagents
7	117	36.2	190	6	BD082137	BD082137 Reagents
8	78	24.1	519	6	BD082142	BD082142 Reagents
9	78	24.1	569	6	AR252648	AR252648 Sequence
10	78	24.1	570	6	AX403520	AX403520 Sequence
11	78	24.1	570	6	BD082138	BD082138 Reagents
12	77	23.8	244	6	BD082138	BD082138 Reagents
13	58	18.0	167634	2	AC143286	AC143286 Macaca mu
14	55.4	17.2	187413	2	AC141871	AC141871 Mus muscu
15	54.8	17.2	210420	2	BX470203	BX470203 Mus muscu
C 16	54.8	17.0	167077	2	AC081093	AC081093 Papio anu
C 17	54.8	17.0	219952	2	AC084804	AC084804 Mus muscu
C 18	54.6	16.9	2685	9	HUMHBA3	HUMHBA3
19	54.6	16.9	43058	6	AX332810	AX332810 Sequence
20	54.6	16.9	43058	6	AX333047	AX333047 Sequence
21	54.6	16.9	43058	6	AX411306	AX411306 Sequence
22	54.6	16.9	43058	6	HSQGI1	HSQGI1
C 23	54.6	16.9	53370	2	AC126375	AC126375 Homo sapi
C 24	54.6	16.9	258002	9	AE006462	AE006462 Homo sapi
C 25	52.6	16.3	1133	9	AF327440	AF327440 Homo sapi
C 26	52.6	16.3	149252	9	AC012615	AC012615 Homo sapi
27	52.4	16.2	135119	2	AC011578	AC011578 Homo sapi
28	52.2	16.2	557	5	XELRGE12	XELRGE12
29	52.2	16.2	3924	5	XELRGE12	XELRGE12
30	52.2	16.2	7634	5	XL28SR	XL28SR
31	52.2	16.2	8153	5	XL28SR	XL28SR
C 32	52.2	16.2	52390	2	AC100946	AC100946 Mus muscu
C 33	52.2	16.2	123865	2	AC144397	AC144397 Rattus no
C 34	52.2	16.2	209257	2	AC123927	AC123927 Mus muscu
C 35	52	16.1	12562	9	AB053232	AB053232 Homo sapi
C 36	52	16.1	87746	9	AC109826	AC109826 Homo sapi
C 37	51.8	16.0	67246	2	AC105035	AC105035 Homo sapi
C 38	51.8	16.0	71032	2	AC084084	AC084084 Homo sapi
C 39	51.8	16.0	171574	2	AC012300	AC012300 Homo sapi
C 40	51.4	15.9	44508	2	AC136063	AC136063 Rattus no
C 41	51.4	15.9	237915	2	AC140280	AC140280 Mus muscu
C 42	51.2	15.9	48144	2	AC069166	AC069166 Homo sapi
C 43	51.2	15.9	113196	9	HS0697K14	HS0697K14
C 44	51	15.8	1007	11	PM3H11G	PM3H11G
C 45	51	15.8	79023	2	AC021951	AC021951 Homo sapi

#### ALIGNMENTS

RESULT 1  
LOCUS AC022095/c  
DEFINITION Homo sapiens chromosome 5 clone CTB-36B8, WORKING DRAFT SEQUENCE,  
13 unordered pieces.  
ACCESSION AC022095  
VERSION AC022095.5 GI:13699618  
KEYWORDS HTGS PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 127488)  
DOE Joint Genome Institute.  
TITLE Sequencing of Human Chromosome 5



```

Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: 16686
Center clone name: 451.H.23
----- Summary Statistics
Sequencing vector: M13. M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 15042 bases at least Q40
Consensus quality: 15924 bases at least Q20
Consensus quality: 163013 bases at least Q20
Insert size: 165247; sum-of-contigs
Quality coverage: 3.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1      1389: contig of 1389 bp in length
*      1390: gap of 100 bp
*      1489: gap of 100 bp
*      1490: contig of 1641 bp in length
*      3131: gap of 100 bp
*      3230: gap of 100 bp
*      3231: contig of 1712 bp in length
*      4942: gap of 100 bp
*      5042: gap of 100 bp
*      5043: contig of 1939 bp in length
*      6981: gap of 100 bp
*      7081: contig of 1627 bp in length
*      7082: gap of 100 bp
*      8708: contig of 1478 bp in length
*      8809: gap of 100 bp
*      8809: contig of 1478 bp in length
*      10387: gap of 100 bp
*      10387: contig of 1826 bp in length
*      12212: gap of 100 bp
*      12212: contig of 2346 bp in length
*      12213: gap of 100 bp
*      14658: contig of 2346 bp in length
*      14659: gap of 100 bp
*      17941: contig of 3183 bp in length
*      17942: gap of 100 bp
*      21297: contig of 3256 bp in length
*      21297: gap of 100 bp
*      21397: contig of 3595 bp in length
*      24992: contig of 3595 bp in length
*      24992: gap of 100 bp
*      25092: gap of 100 bp
*      25092: contig of 2676 bp in length
*      27689: gap of 100 bp
*      27689: contig of 3320 bp in length
*      31189: gap of 100 bp
*      31189: contig of 2426 bp in length
*      31289: gap of 100 bp
*      33714: contig of 2426 bp in length
*      33715: gap of 100 bp
*      37277: contig of 3463 bp in length
*      37277: gap of 100 bp
*      37378: contig of 4925 bp in length
*      42302: gap of 100 bp
*      42302: contig of 5414 bp in length
*      47816: gap of 100 bp
*      47817: contig of 4670 bp in length
*      52587: gap of 100 bp
*      52587: contig of 3881 bp in length
*      56867: gap of 100 bp
*      56867: contig of 4890 bp in length
*      56868: gap of 100 bp
*      61657: contig of 5067 bp in length
*      61658: gap of 100 bp
*      66724: gap of 100 bp
*      66724: contig of 4744 bp in length
*      66825: gap of 100 bp
*      71568: contig of 4910 bp in length
*      71569: gap of 100 bp
*      76578: contig of 6634 bp in length
*      76579: gap of 100 bp
*      83312: contig of 6634 bp in length
*      83313: gap of 100 bp
*      90053: contig of 6641 bp in length
*      90153: gap of 100 bp
*      90154: contig of 9273 bp in length

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*      99427: 99526: gap of 100 bp
*      99527: 108015: contig of 8489 bp in length
*      108016: 108115: gap of 100 bp
*      108116: 118144: contig of 10029 bp in length
*      118145: 118244: gap of 100 bp
*      118245: 130468: contig of 12224 bp in length
*      130469: 142239: gap of 100 bp
*      142240: 142339: gap of 100 bp
*      142340: 157135: contig of 14796 bp in length
*      157136: 157235: gap of 100 bp
*      157236: 168347: contig of 11112 bp in length.
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3231. .4942
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5043. .6981
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7082. .8708
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Consensus quality: 124488 bases at least Q40  
 Consensus quality: 128031 bases at least Q30  
 Consensus quality: 128842 bases at least Q20  
 Estimated insert size: 135000; agarose-fp estimation  
 Estimated insert size: 129829; sum-of-coverage estimation  
 Quality coverage: 7.66 in Q20 bases; agarose-fp estimation  
 Quality coverage: 7.97 in Q20 bases; sum-of-coverage estimation.  
 NOTE: This is a 'working draft' sequence. It currently  
 consists of 4 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 4320: contig of 4320 bp in length  
 \* 4321 4420: gap of unknown length  
 \* 4421 23712: contig of 19392 bp in length  
 \* 23713 23813: gap of unknown length  
 \* 23813 48602: contig of 24790 bp in length  
 \* 48603 48702: gap of unknown length  
 \* 48703 130129: contig of 81427 bp in length.

FEATURES  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="5"  
 /clone="CTD-2013L15"  
 /clone\_lib="Caltech human BAC library D"

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 ORIGIN

Query Match 94.4%; Score 304.8; DB 2; Length 130129;  
 Best Local Similarity 99.1%; Pred. No. 1e-45; 2; Indels 1; Gaps 1;

Matches 317; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GCGCGTGGGTCAAGACCGCAAGCGAAGGTGCGGGCGGGGTGGGCTTCGCGAGACAA 60  
 DB 24359 GCGCGTGGGTCAAGACCGCAAGCGAAGGTGCGGGCGGGGTGGGCTTCGCGAGACAA 24300  
 QY 61 GCGCGGCTGCTCTCTCAAGAGGCGCCAGCGCTTCGCAAGAGAAAGTCTTCAGAGCC 119  
 DB 24299 GCGCGGCTGCTCTCTCAAGAGGCGCCAGCGCTTCGCAAGAGAAAGTCTTCAGAGCC 24240  
 QY 120 CCGGCGAGGAGAGGGGCGACGCGCTTCCAGAGGCGCCGCGCGCGAGAGAGAGTTGGCCA 179  
 DB 24239 CCGGCGAGGAGAGGGGCGACGCGCTTCCAGAGGCGCCGCGCGCGAGAGAGTTGGCCA 24180  
 QY 180 GCGCAAGCGCGTGAAGCGAGCGGCGGCTTCTCAGAGAGCGGCGAGGCGCGCGCT 239  
 DB 24179 GCGCAAGCGCGTGAAGCGAGCGGCGGCTTCTCAGAGAGCGGCGAGGCGCGCGCT 24120  
 QY 240 GAGAGGCGAGAGACCGGCTATAGAAAGCTCGTGCGCTTGGCGGCGAGCGCGAGTTCC 299  
 DB 24119 GAGAGGCGAGAGACCGGCTATAGAAAGCTCGTGCGCTTGGCGGCGAGCGCGAGTTCC 24060  
 QY 300 CCGCGCGCGCGAGGCGCGCG 319  
 DB 24059 CCGCGCGCGCGAGGCGCGCG 24040

RESULT 5  
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 LOCUS Homo sapiens chromosome 5 clone RP11-586L9, WORKING DRAFT SEQUENCE,  
 DEFINITION 3 Homologous pieces.  
 AC106813 3 GI:19224876  
 ACCESSION AC106813 3 GI:19224876  
 VERSION HTG; HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 166777)  
 DOE Joint Genome Institute.  
 Sequencing of Human Chromosome 5  
 Unpublished  
 2 (bases 1 to 166777)  
 DOE Joint Genome Institute.  
 Direct Submission  
 Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 3 (bases 1 to 166777)  
 DOE Joint Genome Institute.  
 Direct Submission  
 Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 On Mar 7, 2002 this sequence version replaced gi:18369924.  
 -----Genome Center  
 Center: Joint Genome Institute  
 Center Code: JGI  
 Web site: http://www.jgi.doe.gov

Project Information  
 Center Project Name: 1519801  
 Center clone name: RP11-586L9

Summary Statistics  
 Consensus quality: 163497 bases at least Q40  
 Consensus quality: 166071 bases at least Q30  
 Consensus quality: 166432 bases at least Q20  
 Estimated insert size: 166250; agarose-fp estimation  
 Estimated insert size: 166577; sum-of-coverage estimation  
 Quality coverage: 9.4 in Q20 bases; agarose-fp estimation  
 Quality coverage: 10.51 in Q20 bases; sum-of-coverage estimation.  
 NOTE: This is a 'working draft' sequence. It currently  
 consists of 3 contigs. Gaps between the contigs  
 are represented as runs of N. The order of the pieces  
 is believed to be correct as given, however the sizes  
 of the gaps between them are based on estimates that have  
 been provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.

## FEATURES

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 /db\_xref="taxon:9606"  
 /chromosome="5"  
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 Matches 323; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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 QY 61 GCGCGGCTGCTCTCTCAAGAGGCGCCAGCGCTTCGCAAGAGAAAGTCTTCAGAGCC 119  
 DB 119374 GCGCGGCTGCTCTCTCAAGAGGCGCCAGCGCTTCGCAAGAGAAAGTCTTCAGAGCC 119433  
 QY 120 CCGGCGAGGAGAGGGGCGACGCGCTTCCAGAGGCGCCGCGCGCGAGAGAGTTGGCCA 179  
 DB 119434 CCGGCGAGGAGAGGGGCGACGCGCTTCCAGAGGCGCCGCGCGCGAGAGAGTTGGCCA 119493

RESULT 6  
LOCUS BD082141 562 bp DNA linear PAT 27-AUG-2002  
DEFINITION Reagents and methods useful for detecting diseases of the lung.  
ACCESSION BD082141.1 GI:22627751  
VERSION JP 2001522225-A/5.  
KEYWORDS Zea mays  
SOURCE Zea mays  
ORGANISM Zea mays  
REFERENCE Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,  
AUTHORS Granados,E.N., Hodges,S.C., Klaas,M.R., Kratochvil,J.D., Rapp,L.R.,  
TITLE Russell,J.C. and Stroupe,S.D.  
JOURNAL Reagents and methods useful for detecting diseases of the lung  
PATENT: JP 2001522225-A 5 13-NOV-2001;  
ABBOTT LABORATORIES  
COMMENT PN JP 2001522225-A/5  
PI 13-NOV-2001  
PF 30-JAN-1998 JP 1998533078  
PR 31-JAN-1997 US 08/791710  
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA  
N FRIEDMAN,  
PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI  
KLAAS,  
PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D  
PI STROUPE  
PC C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC  
Strandness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:4577"  
BASE COUNT 82 a 200 c 192 g 86 t 2 others  
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Best Local Similarity 99.2%; Pred. No. 4, 4e-12;  
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 203 GCAGGCTTTCTCAGAGGCGGCGAGGCGCGCTGTGAGGGGCGAGGACCGGGTATTA 262  
DB 1 GCAGGCTTTCTCAGAGGCGGCGAGGCGCGCTGTGAGGGGCGAGGACCGGGTATTA 60  
OY 263 GAAGCTCTGTGGCTTGTCCCGGCGACCGCAGATTCCCGCGCGCCCGAGCCCGCGGC 322  
DB 61 GAAGCTCTGTGGCTTGTCCCGGCGACCGCAGATTCCCGCGCGCCCGAGCCCGCGGC 120  
OY 323 C 323  
DB 121 C 121

RESULT 7  
LOCUS BD082137 190 bp DNA linear PAT 27-AUG-2002  
DEFINITION Reagents and methods useful for detecting diseases of the lung.  
ACCESSION BD082137.1 GI:22627747  
VERSION JP 2001522225-A/1.  
KEYWORDS Zea mays  
SOURCE Zea mays  
ORGANISM Zea mays  
REFERENCE Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,  
AUTHORS Granados,E.N., Hodges,S.C., Klaas,M.R., Kratochvil,J.D., Rapp,L.R.,  
TITLE Russell,J.C. and Stroupe,S.D.  
JOURNAL Reagents and methods useful for detecting diseases of the lung  
PATENT: JP 2001522225-A 1 13-NOV-2001;  
ABBOTT LABORATORIES  
COMMENT PN JP 2001522225-A/1  
PI 13-NOV-2001  
PF 30-JAN-1998 JP 1998533078  
PR 31-JAN-1997 US 08/791710  
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA  
N FRIEDMAN,  
PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI  
KLAAS,  
PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D  
PI STROUPE  
PC C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC  
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CC Topology: Linear;  
FH Key Location/Qualifiers.  
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Matches 117; Conservative 0; Mismatches 4;  
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DB 1 GCAGGCTTTCTCAGAGGCGGCGGAGGCGCGCTGTGAGGGGCGAGGACCGGGTATTA 60  
OY 263 GAAGCTCTGTGGCTTGTCCCGGCGACCGCAGATTCCCGCGCGCCCGAGCCCGCGGC 322  
DB 61 GAAGCTCTGTGGCTTGTCCCGGCGACCGCAGATTCCCGCGCGCCCGAGCCCGCGGC 120  
OY 323 C 323  
DB 121 C 121  
RESULT 8  
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DEFINITION Reagents and methods useful for detecting diseases of the lung.  
ACCESSION BD082142.1 GI:22627752  
VERSION JP 2001522225-A/6.  
KEYWORDS Zea mays  
SOURCE Zea mays  
ORGANISM Zea mays  
REFERENCE Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,  
AUTHORS Granados,E.N., Hodges,S.C., Klaas,M.R., Kratochvil,J.D., Rapp,L.R.,  
TITLE Russell,J.C. and Stroupe,S.D.  
JOURNAL Reagents and methods useful for detecting diseases of the lung  
PATENT: JP 2001522225-A 6 13-NOV-2001;  
ABBOTT LABORATORIES  
COMMENT PN JP 2001522225-A/6  
PI 13-NOV-2001  
PF 30-JAN-1998 JP 1998533078  
PR 31-JAN-1997 US 08/791710  
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA  
N FRIEDMAN,  
PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI  
KLAAS,  
PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D  
PI STROUPE  
PC C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC  
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OY 323 C 323  
DB 121 C 121

Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R., Russell, J.C., and Strupe, S.D.  
Reagents and methods useful for detecting diseases of the lung  
Patent: JP 2001522225-A 6 13-NOV-2001;  
ABBOTT LABORATORIES  
PN JP 2001522225-A/6  
PD 13-NOV-2001  
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PI N FRIDMAN,  
PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI  
PI KLAS,  
PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D  
PI STROUPE  
PI C12N15/63, C12N5/10, C1201/68, C07K14/47//C07K16/30, G01N33/574 CC  
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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE  
1 Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Hillan, R.J., Marsters, S.A., Pan, J., Piltl, R.M., Roy, M.A., Smith, V.,  
Stone, D.M., Watanabe, C.K., and Wood, W.I.  
Compositions and methods for the treatment of tumour  
Patent: WO 0153486-A 27 26-JUL-2001;  
Genentech, Inc. (US)  
LOCATION/Qualifiers  
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Unclassified.  
1 (bases 1 to 570)  
Wintebottom, J.M., Shimp, L., Boyce, T.M., and Kaes, D.  
Implant, method of making same and use of the implant for the  
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Patent: US 6478825-A 407 12-NOV-2002;  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D.,  
Ferrara, N., Gerber, H., Gerltzen, M., Goddard, A., Godowski, P.,  
Grimaldi, C.J., Gurney, A.L., Klavin, I., Napier, M.A., Pan, J.,  
Pooni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
Williams, P., Wood, W.I., and Zhang, Z.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
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Patent: WO 0073454-A 407 07-DEC-2000;  
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[illegible]

Fri Nov 7 08:10:01 2003

us-10-081-817a-19\_copy\_229\_551.rge

Page 12

AUTHORS Green, E.D.  
TITLE Direct Submission  
JOURNAL Submitted (29-MAR-2001) NIH Intramural Sequencing Center, 8717  
Govermont Circle, Gaithersburg, MD 20877, USA

Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: <http://www.nisc.nih.gov>  
Contact: [nisc\\_mouse@nigl.nih.gov](mailto:nisc_mouse@nigl.nih.gov)  
Project Information  
Center project name: amz  
Center clone name: 333P04

Summary Statistics  
Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 164327 bases at least Q40  
Consensus quality: 164859 bases at least Q30  
Consensus quality: 165145 bases at least Q20  
Insert size: 135000; agarose-fp  
Insert size: 14000; pulse-field-gel  
Insert size: 16677; sum-of-ctnigs  
Quality coverage: 9.16x in Q20 bases; agarose-fp  
Quality coverage: 8.59x in Q20 bases; pulse-field-gel  
Quality coverage: 7.42x in Q20 bases; sum-of-ctnigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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\* 65712 65811: gap of unknown length  
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2 CGCGTGGGTCAACCGCAAGGAGGTGCGCGGCTCCGCGAGCAAG 61  
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Qy 122 GCGAGGAAAGGAGGCGCGCGCTTCCAGAGGCGCGCGCGCGCGCGAGCAAGAGTTCGAGG 181  
Db 166801 CGCGCGGGGCGCGCGGAGCGCGCGCGGGGAGGGGGGCGGGGCGCGCGCGAGCAAGC 166742  
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Qy 302 GCGCGCGCGCGAGCGCG 316  
Db 166621 GCGCGCGAGAGCGCG 166607

RESULT 17  
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DEFINITION Mus musculus clone RP23-314K21 strain C57BL6/J, WORKING DRAFT  
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VERSION AC084804.10 GI:17488575  
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 219952)  
Grill's G., Han, J., Montgomery, K.T., Chiu, D., Decker, J., Fusina, M.,  
Goltz, J., Haider, A., Hall, L., Ioshikhes, I.P., Lee, E., Long, J.,  
Perera, A., Shim, C., Thomas, E. and Kuchertapatti, R.  
High Throughput Mouse Sequencing  
Unpublished  
2 (bases 1 to 219952)  
Grill's G., Han, J., Montgomery, K.T., Chiu, D., Decker, J., Fusina, M.,  
Goltz, J., Haider, A., Hall, L., Ioshikhes, I.P., Lee, E., Long, J.,  
Perera, A., Shim, C., Thomas, E. and Kuchertapatti, R.  
Direct Submission  
Submitted (18-NOV-2000) Department of Molecular Genetics, Albert  
Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,  
Bronx, NY 10461, USA  
On Dec 11, 2001 this sequence version replaced gi:13560369.  
TITLE AC084804  
JOURNAL  
AUTHORS  
REFERENCE  
COMMENT

Center: Harvard Partners Genome Center  
Center Code: HPGC  
Web site: <http://www.hpcg.org/Sequence/mouse.html>  
Contact: [hpgc@mdel.mgh.harvard.edu](mailto:hpgc@mdel.mgh.harvard.edu)  
-----Summary Statistics  
Center project name: AEZ  
Sequencing vector: pUC18; L08752  
Chemistry: Dye-terminator Big Dye; 100%  
\*Consensus quality: 207914 at least Q20  
\*Consensus quality: 205077 at least Q30  
\*Consensus quality: 200559 at least Q40  
\*Estimated insert size: agarose-fp - N/A  
\*Estimated insert size: 219052 - sum-of-ctnigs  
Quality coverage: 10.7 x in Q20 bases; sum-of-ctnigs estimation  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 46 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence



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* as soon as it is available and the accession number will
* be preserved.
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208451: gap of unknown length
209852: contig of 1382 bp in length
209853: gap of unknown length
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210569: contig of 697 bp in length
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210757: contig of 168 bp in length
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211360: contig of 583 bp in length
211361: gap of unknown length
211510: contig of 130 bp in length
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212467: contig of 917 bp in length
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* 214401 214420: gap of unknown length
* 214421 214977: contig of 537 bp in length
* 214978 214979: gap of unknown length
* 214979 215140: contig of 163 bp in length
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* 215161 215345: contig of 185 bp in length
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* 215366 216233: contig of 868 bp in length
* 216234 216283: gap of unknown length
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* 216820 216839: gap of unknown length
* 216840 219659: contig of 2820 bp in length
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				25861	GCCCCCGCATGAGCGCCCC	25861
					Accession 284721 GI:1817575	
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					SOURCE Homo sapiens (human)	
					ORGANISM Homo sapiens	
					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
					REFERENCE 1 (bases 1 to 43058) Flint J. and Higgs D.R.	
					TITLE Direct Submission Submitted (28-JAN-1997) Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, UK. E-mail enquiries: humpub@sanger.ac.uk	
					JOURNAL IMPORTANT: This sequence is the entire insert of clone GGI. This clone was sequenced at the Institute of Molecular Medicine. The true left end of clone GGI is at 1 in this sequence. The true right end of clone GGI is at 43058.	
					GGI is from a 280kb clone confg extending from the telomere of 16p. Higgs D.R., Flint J. unpublished. MRC Molecular Haematology Unit, Institute of Molecular Medicine, Oxford.	
					GGI came from the Los Alamos, flow sorted human Chromosome 16 library.	
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VERSION	AC126375.1	GI:21699326	
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ORGANISM	Homo sapiens		
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AUTHORS	Blumen, B., Nusbaum, C. and Lander, E.		
TITLE	Homo sapiens chromosome 18, clone CTD-2333M9		
JOURNAL	Unpublished		
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AUTHORS	Blaum, N., Blaum, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Chazaro, K., Chepel, Y., Collymore, A., Cook, A., Cooke, P., Daxellano, R., Dewar, K., Diaz, U.S., Dodge, S., Farooq, S., Ferreira, P., Fitzgerald, W., Gage, D., Galagan, J., Gardyna, S., Gerold, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karstens, A., Kelly, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Menais, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rice, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schnuppback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stangor-Tromann, N., Stojanovic, N., Talmas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vaasiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zemek, L., Zimmer, A. and Zody, W.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
COMMENT	All repeats were identified using RepeatMasker: Smith, A.P.A. & Green, P. (1996-1997) <a href="http://ftp.genome.washington.edu/MN/RepeatMasker.html">http://ftp.genome.washington.edu/MN/RepeatMasker.html</a>		
	Center: Whitehead Institute/MIT Center for Genome Research Web site: <a href="http://www-seg.wi.mit.edu">http://www-seg.wi.mit.edu</a> Contact: <a href="mailto:sequence_submissions@genome.wi.mit.edu">sequence_submissions@genome.wi.mit.edu</a> Project Information Center Project name: L27663 Center Clone name: 2333_M9		
* NOTE:	This record contains 66 individual sequencing reads that have not been assembled into		

\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlaid relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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#### FEATURES

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AUTHORS	1 (bases 2 to 258002) Flint,J., Thomas,K., Micklem,G., Raynham,H., Clark,K., Doggett,N.A., King,A. and Higgs,D.R.
TITLE	The relationship between chromosome structure and function at a human telomeric region
JOURNAL	Nat. Genet. 15 (3), 252-257 (1997)
PUBLISHED	97207643
REFERENCE	2 (bases 1 to 258002) Danteis,R.J., Peden,J.F., Lloyd,C., Horsley,S.W., Clark,K., Tufarelli,C., Kearney,L., Buckle,V.J., Doggett,N.A., Flint,J. and Higgs,D.R.
AUTHORS	Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16
TITLE	Hum. Mol. Genet. 10 (4), 339-352 (2001)
JOURNAL	21096910
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QY 183 CAGCGCGTGAAGCGAGCGGCGAGGCTTCTCAGAGCGCGCGCGCGCTGGA 242  
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QY 243 GGGGCGAGAGCGCGGTATTAAGAGCTCTGTGCGCTTGGCGCGAGCGCGAGTTCCCG 302  
DB 172 GCCCGCGGCTCCCGGTGAGCGCGCTCGCGCGCGCGCGCGCAGTCAGCGCGCG 113  
QY 303 CGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 323  
DB 112 CGGCG 92

RESULT 26  
AC012615 149252 bp DNA linear PRI 03-AUG-2002  
LOCUS Homo sapiens chromosome 19 clone CTB-31020, complete sequence.  
DEFINITION  
AC012615  
VERSION AC012615.4 GI:22094313  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 149252)  
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.  
REFERENCE  
AUTHORS Unpublished  
JOURNAL 2 (bases 1 to 149252)  
TITLE DOE Joint Genome Institute.  
AUTHORS Direct Submissions  
JOURNAL Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
3 (bases 1 to 149252)  
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.  
REFERENCE  
AUTHORS Direct Submissions  
JOURNAL Submitted (03-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
COMMENT On Aug 3, 2002 this sequence version replaced gi:7711554.

Draft Sequence Produced by DOE Joint Genome Institute  
www.jgi.doe.gov  
finishing completed at Stanford Human Genome Center  
www.sbgc.stanford.edu  
Quality: Phrap Quality >=40.99.8% of Sequence;  
Estimated Total Number of Errors is 0.5  
NOTE: BACTERIAL TRANSPOSON excised at 118353.

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1. 149252  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="19"  
/clone="CTB-31020"

BASE COUNT 31733 a 44198 c 44336 g 28985 t

ORIGIN

Query Match 16.3%; Score 52.6; DB 9; Length 149252;  
Best Local Similarity 49.8%; Pred. No. 1.4;  
Matches 160; Conservative 0; Mismatches 159; Indels 2; Gaps 1;

QY 3 GCGTGGGTCAGACCGCAAGAGAGTGCAGGCGGAGGCTCGCGAGACAAAG 62  
DB 55535 GCTTGGCGCAGTCCCGAAGAGAGACAGCGGTCTTGGCGGCGAGGCGCGCG 55594  
QY 63 CCGGCGCTCTCTCTCAGAGGCGCCAGCGCTCGACAGAGTCTCGAGCGCG 122  
DB 55595 CCGGCGCGCGCGCCAGAGCGAGCGCGCTGAGAGAGAGCGCGCGAGCG 55654  
QY 123 GCAGGAGAGGAGCGAGCGCTTCCAGGCGCGCGCGCGAGAGATTGGCAGG 182  
DB 55655 CCGCGGAGCGCGCTCGAGTCCGCGCGAGTGGC--CAGATGCTGCGCGCAGCA 55712  
QY 183 CAGCGCGTGAAGCGAGCGGCGAGGCTTCTCAGAGCGCGCGCGCGCTGGA 242  
DB 55713 GGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTG 55772  
QY 243 GGGGCGAGAGCGCGGTATTAAGAGCTCTGTGCGCTTGGCGCGAGCGCGAGTTCCCG 302  
DB 55773 GCCCGCGGCTCCCGGTGAGCGCGCTCGCGCGCGCGCGCGCAGTCAGCGCGCG 55832  
QY 303 CGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 323  
DB 55833 CGGCG 92

RESULT 27  
AC011578 135119 bp DNA linear HTG 13-JUL-2000  
LOCUS Homo sapiens clone RP11-12P9, LOW-PASS SEQUENCE SAMPLING.  
DEFINITION  
AC011578  
VERSION AC011578.4 GI:9123847  
KEYWORDS HTG; HTGS-PHASE0.  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 135119)  
TITLE Homo sapiens, clone RP11-12P9  
REFERENCE  
AUTHORS Unpublished  
JOURNAL 2 (bases 1 to 135119)  
TITLE Nussbaum, C., Lander, E., Allen, N., Anderson, M.,  
Baldwin, J., Barina, N., Beckerly, R., Boguslavsky, L., Bouhgalier, B.,  
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,  
Cooke, P., Dearellano, K., Dewar, K., Domingo, M., Donelan, L., Doyle, M.,  
Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,  
Galligan, J., Gardina, S., Grant, G., Hagos, B., Heath, A., Horton, L.,  
Hawland, J., Johnson, R., Jones, C., Kann, L., Karas, A., Kerton, D.,  
Lehoczky, J., Lieu, C., Locke, K., MacDonald, P., Margulis, N.,  
McEwan, P., McGurk, A., McKernan, K., McDonald, J., Meltrin, J.,  
Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

TITLE  
JOURNAL  
COMMENT

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talama, J.,  
Testa, S., Tittel, A., Vasilev, H., Vo, A., Wheeler, J., Wu, X.,  
Wymann, D., Ye, W. J., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (07-OCT-1999) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:17107923.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: MIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: sequence\_submission@genome.wi.mit.edu  
Project Information  
Center project name: L3313  
Center clone name: L2\_P\_9

NOTE: This record contains 146 individual  
sequencing reads that have not been assembled into  
contigs. Runs of N are used to separate the reads  
and the order in which they appear is completely  
arbitrary. Low-pass sequence sampling is useful for  
identifying clones that may be gene-rich and allows  
overlap relationships among clones to be deduced.  
However, it should not be assumed that this clone  
will be sequenced to completion. In the event that  
the record is updated, the accession number will  
be preserved.

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1616 1715: gap of 100 bp  
1716 2485: contig of 770 bp in length  
2486 2585: gap of 100 bp  
2586 3345: contig of 760 bp in length  
3346 4188: gap of 100 bp  
4189 4288: contig of 743 bp in length  
4289 5020: gap of 100 bp  
5021 5150: contig of 762 bp in length  
5151 5984: gap of 100 bp  
5985 6084: contig of 834 bp in length  
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6838 6937: gap of 100 bp  
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36887 37722: contig of 736 bp in length  
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42013 42781: contig of 769 bp in length  
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47062 47161: gap of 100 bp  
47162 47915: contig of 754 bp in length  
47916 48015: gap of 100 bp  
48016 48759: contig of 744 bp in length  
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[illegible]

JOURNAL	Nucleic Acids Res.	11 (3)	629-646 (1983)
MEJLINE	83168891		
PUBMED	6300760		
COMMENT	Original source text: Xenopus laevis DNA, clone pX1101.		
FEATURES	<p>source</p> <p>1.557</p> <p>location/Qualifiers</p> <p>organism="Xenopus laevis"</p> <p>molecule="genomic DNA"</p> <p>taxon="Xenopus laevis"</p>		
BASE COUNT	69 a	239 c	230 g 19 t
ORIGIN			
Query Match	16.2%	Score 52.2;	DB 5; Length 557;
Best Local Similarity	50.5%	Pred. No. 6.2;	Mismatches 148; Indels 1; Gaps 1
Matches 152;	Conservative	0;	
23	GCAGAGGTGCGGCGCGGCTTCCGCGAGACAAAGCCGCGCTCTCTTCAGA	82	
158	GCAGAGGAGGCGGCGCGCGCGCGGCTTCCAGCCCGGCGCGCTTCCCGCGC	217	
83	GGGCGCCAGCGCTTGCAGAGAAATCTTCAGAGCCCGGCGAGGAGGCGACCGGC	142	
218	GGGCGCGCGCGCGGCTTACCTTACCGCG -GGCGCGGCGCGCGGCGCTTGCAGGAGCGGCGC	276	
143	TTCCCGAGGCGCGCGCGCGCGCGAGCAAGTTTGGCGAGGCGACCGCGTGAAGCGGCG	202	
277	GCCCGAGGCGCGCGCGCGCTTCCCGCGCTTCCCGCGAGCCGCGCGCGGCGGTTTCA	336	
203	GCGAGGCTTTCTAGAGAGCGCGGCGAGCGCGCGCTTGAAGGCGAGACCGGCTTTAA	262	
337	AGACCCCGCGCGCGCGCGCGCGGAGGCGCGGAGAGGAGCGCGGAGGAGGAGGAGG	396	
263	GAGAGCTTCTTGGCGCTTGGCGCGCGCGCGCGAGGTTCCCGCGCGCGCGCGCGCGC	322	
397	GCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGAGACCCCGCTTCCCGCGCGCGC	456	
QY	323 C 323		
QY	457 C 457		
RESULT 29			
LOCUS	XELRGE812	3924 bp	DNA linear VRT 28-APR-199
DEFINITION	x.laevis external transcribed spacer (ets) & 18S, 5.8S, 28S (5', end) rRNA genes; clone pX1101.		
ACCESSION	J000999.1	GI:214711	
KEYWORDS	18S ribosomal RNA; 28S ribosomal RNA; 5.8S ribosomal RNA; external transcribed spacer; ribosomal RNA.		
SEGMENT	2 of 2		
ORGANISM	Xenopus laevis (African clawed frog)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.		
AUTHORS	1. (bases 977 to 1275) Salim,M. and Maden,B.E.		
TITLE	Nucleotide sequence encoding the 5' end of Xenopus laevis 18S rRNA		
REFERENCE	81053719 Nucleic Acids Res. 8 (13), 2871-2884 (1980)		
AUTHORS	2. (bases 2599 to 3924) Hall, L.M. and Maden, B.E.		
TITLE	Nucleotide sequence through the 18S-28S intergene region of a vertebrate ribosomal transcription unit		
REFERENCE	6258158 Nucleic Acids Res. 8 (24), 5935-6005 (1980)		
AUTHORS	3. (bases 1001 to 2825) Salim,M. and Maden,B.E.		
TITLE	Nucleotide sequence of Xenopus laevis 18S ribosomal RNA inferred from gene sequence		

JOURNAL Nature 291 (5812), 205-208 (1981)  
MEDLINE 81197642  
PubMed 7015146  
REFERENCE 4 (bases 1 to 1060)  
AUTHORS Maden,B.E., Moss,M. and Salim,M.  
TITLE Nucleotide sequence of an external transcribed spacer in Xenopus laevis rDNA: sequences flanking the 5' and 3' ends of 18S rRNA are non-complementary  
JOURNAL Nucleic Acids Res. 10 (7), 2387-2398 (1982)  
MEDLINE 82221416  
PubMed 6283480  
COMMENT Original source text: xenopus laevis dna; clone px1r101 [Nucleic Acids Res. 8, 2871-2884 (1980)], [2], [3], [4].  
[3] comparison with s.cerevisiae 18S rDNA revealed extensive regions of high homology interspersed with tracts having little or no homology. regions of high homology contain almost all the rna methyl groups. major regions of low homology are considerably richer in 'c' and 'g' in xenopus than in the yeast [3]. [4] found that there are not initiation (atg) codons in the ets region and that, as in other x.laevis rDNA clones, the sequence preceding the ets is duplicated, with a few changes, in the 'bam island' sequence of the non-transcribed spacer.  
location/Qualifiers

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289..3924  
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/note="[14] uncertain about 'g' string length"  
1001..2825  
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3383..3544  
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ORIGIN 163 bp upstream of hinfI site.

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Best Local Similarity 50.5%; Pred. No. 3.9;  
Matches 152; Conservative 0; Mismatches 148; Indels 1; Gaps 1;

QY 23 GCGAAGGTGCGGCGCGGCTGCGGAGCAAGAGCCGCGCTGCTCTCTCA 82  
DB 2983 GCGAAGGTGCGGCGCGGCTGCGGAGCAAGAGCCGCGCTGCTCTCTCA 3042  
QY 83 GGGCCCCAGGCTGCGAAGAGTCTCGAGCCCGGAGGAGAGGGGCAACG 142  
DB 3043 GGGCCCCAGGCTGCGAAGAGTCTCGAGCCCGGAGGAGAGGGGCAACG 3101  
QY 143 TTCCAGAGGCGCGCGCGCGAGAGAGTTGGCCAGGCAACGCGCTGAGCGAGCG 202  
DB 3102 GCGGAGGCGCGCGCGCGCGAGAGAGTTGGCCAGGCAACGCGCTGAGCGAGCG 3161  
QY 203 GCAGGCTTTCTAGAGAGCGCGGCAAGCCGCTGAGAGGGGAGAGACCGGGTATA 262  
DB 3162 AGACCCCGCGCGCGCGCGAGAGAGCGGAGAGAGCGGAGAGAGGGGAGAG 3221  
QY 263 GAAGCTCTGAGCTTGGCCCGGAGCGGAGAGTTCCCGCGCGCGCGAGCCCGCG 322  
DB 3222 GCGGCGGAGCGCGCGCGCGAGAGCGGAGAGTTCCCGCGCGCGCGAGCCCGCG 3281  
QY 323 C 323  
DB 3282 C 3282

RESULT 30  
X128SR

LOCUS XL28SR 7634 bp DNA linear VRT 06-JUN-2003  
DEFINITION X.laevis 28S ribosomal RNA gene for 28S rRNA.  
ACCESSION X59734  
VERSION X59734.1 GI:64487  
KEYWORDS 18S ribosomal RNA; 28S ribosomal DNA; 40S ribosomal subunit; 5.8S ribosomal DNA; ribosomal RNA transcription unit.  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.  
1 (bases 1 to 7634)  
Xenopus borealis and Xenopus laevis 28S ribosomal DNA and the complete 40S ribosomal precursor RNA coding units of both species  
Proc. R. Soc. Lond., B, Biol. Sci. 245 (1312), 65-71 (1991)  
92052296  
location/Qualifiers

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/note="internal transcribed spacer 2"  
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BASE COUNT 1379 a 2461 c 2610 g 1184 t  
ORIGIN

Query Match 16.2%; Score 52.2; DB 5; Length 7634;  
Best Local Similarity 50.5%; Pred. No. 3.4; 148; Indels 1; Gaps 1;  
Matches 152; Conservative 0; Mismatches 148; Indels 1; Gaps 1;

QY 23 GCGAAGGTGCGGCGCGGCTGCGGAGCAAGAGCCGCGCTGCTCTCTCA 82  
DB 2696 GCGAAGGTGCGGCGCGGCTGCGGAGCAAGAGCCGCGCTGCTCTCTCA 2755  
QY 83 GGGCCCCAGGCTGCGAAGAGTCTCGAGCCCGGAGGAGAGGGGCAACG 142  
DB 2756 GGGCCCCAGGCTGCGAAGAGTCTCGAGCCCGGAGGAGAGGGGCAACG 2814  
QY 143 TTCCAGAGGCGCGCGCGCGAGAGAGTTGGCCAGGCAACGCGCTGAGCGAGCG 202  
DB 2815 GCGGAGGCGCGCGCGCGCGAGAGAGTTGGCCAGGCAACGCGCTGAGCGAGCG 2874  
QY 203 GCAGGCTTTCTAGAGAGCGCGGCAAGCCGCTGAGAGGGGAGAGACCGGGTATA 262  
DB 2875 AGACCCCGCGCGCGCGCGAGAGAGCGGAGAGAGCGGAGAGAGGGGAGAG 2934  
QY 263 GAAGCTCTGAGCTTGGCCCGGAGCGGAGAGTTCCCGCGCGCGCGAGCCCGCG 322  
DB 2935 GCGGCGGAGCGCGCGCGCGAGAGCGGAGAGTTCCCGCGCGCGAGCCCGCG 2994  
QY 323 C 323  
DB 2995 C 2995

RESULT 31  
 LOCUS XLRN01 8153 bp DNA linear VRT 01-OCT-1996  
 DEFINITION Xenopus laevis genes for 18S, 5.8S and 28S ribosomal RNAs.  
 ACCESSION X02995 J00999 J01001 J01002 J01003 J01006 J01007 K01369 K01370  
 K01371 K01372 K01373 K01376 K01535 V01444 V01445 V01446 V01447  
 V01448 V01449 V01450 V01451 V01452 V01453 V01454 V01456 X00136  
 X01071  
 VERSION X02995.1 GI:65056  
 KEYWORDS 18S ribosomal RNA; 28S ribosomal RNA; 5.8S ribosomal RNA;  
 repetitive sequence; ribosomal RNA.  
 SOURCE Xenopus laevis (African clawed frog)  
 ORGANISM Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 Xenopodinae; Xenopus.  
 REFERENCE 1 (bases 1 to 24)  
 Bosseley, P., Moss, T., Machler, M., Portmann, R. and Birnstiel, M.  
 Nucleotide sequence of the spacer DNA in a ribosomal gene unit of  
 Xenopus laevis  
 JOURNAL MEDLINE 79211270  
 CELL 17 (1), 19-31 (1979)  
 PUBMED 455459  
 2 (bases 25 to 1029)  
 Maden, B.E., Moss, M. and Salim, M.  
 Nucleotide sequence of an external transcribed spacer in Xenopus  
 laevis rDNA: sequences flanking the 5' and 3' ends of 18S rRNA are  
 non-complementary  
 JOURNAL MEDLINE 82221416  
 NUCLEIC ACIDS RES. 10 (7), 2387-2398 (1982)  
 PUBMED 6283480  
 3 (bases 1030 to 2854)  
 Salim, M. and Maden, B.E.  
 Nucleotide sequence of Xenopus laevis 18S ribosomal RNA inferred  
 from gene sequence  
 NATURE 291 (5812), 205-208 (1981)  
 JOURNAL MEDLINE 81197642  
 PUBMED 7015146  
 4 (bases 2855 to 3953)  
 Hall, L.M. and Maden, B.E.  
 Nucleotide sequence through the 18S-28S intergene region of a  
 vertebrate ribosomal transcription unit  
 NUCLEIC ACIDS RES. 8 (24), 5993-6005 (1980)  
 JOURNAL MEDLINE 81124313  
 PUBMED 6258158  
 5 (bases 3954 to 7917)  
 Ware, V.C., Tague, B.W., Clark, C.G., Gourse, R.L., Brand, R.C. and  
 Gerbi, S.A.  
 Sequence analysis of 28S ribosomal DNA from the amphibian Xenopus  
 laevis  
 JOURNAL MEDLINE 84069805  
 NUCLEIC ACIDS RES. 11 (22), 7795-7817 (1983)  
 PUBMED 6359063  
 6 (bases 7918 to 8153)  
 Solinger, Webb, B. and Reeder, R.H.  
 The nucleotide sequence of the initiation and termination sites for  
 ribosomal RNA transcription in X. laevis  
 CELL 18 (2), 485-499 (1979)  
 JOURNAL MEDLINE 80045030  
 PUBMED 498280  
 7 (bases 1 to 8153)  
 Moss, T., Bosseley, P.G. and Birnstiel, M.L.  
 More ribosomal spacer sequences from Xenopus laevis  
 NUCLEIC ACIDS RES. 8 (3), 467-485 (1980)  
 JOURNAL MEDLINE 81076644  
 PUBMED 7003549  
 8 (bases 1 to 8153)  
 Salim, M. and Maden, B.E.  
 Nucleotide sequence encoding the 5' end of Xenopus laevis 18S rRNA  
 JOURNAL MEDLINE 81053719  
 NUCLEIC ACIDS RES. 8 (13), 2871-2884 (1980)

PUBMED 6253895  
 9 (bases 1 to 8153)  
 REFERENCE Stewart, M.A., Hall, L.M. and Maden, B.E.  
 Multiple heterogeneities in the transcribed spacers of ribosomal  
 DNA from Xenopus laevis  
 NUCLEIC ACIDS RES. 11 (3), 629-646 (1983)  
 JOURNAL MEDLINE 83168891  
 PUBMED 6300760  
 10 (bases 1 to 8153)  
 REFERENCE Maden, B.E., Forbes, J.M., Stewart, M.A. and Eason, R.  
 18S coding sequences in amplified ribosomal DNA from Xenopus laevis  
 oocytes are highly homogeneous, unmethylated, and lack major open  
 reading frames  
 EMBO J. 1 (5), 597-601 (1982)  
 JOURNAL MEDLINE 84236020  
 PUBMED 6329693  
 11 (bases 1 to 8153)  
 REFERENCE Bosseley, P.G., Tuyns, A. and Birnstiel, M.L.  
 Mapping of the Xenopus laevis 5.8S rDNA by restriction and DNA  
 sequencing  
 NUCLEIC ACIDS RES. 5 (4), 1121-1137 (1978)  
 JOURNAL MEDLINE 78178358  
 PUBMED 652517  
 12 (bases 1 to 8153)  
 REFERENCE Ford, P.J. and Mathieson, T.  
 The nucleotide sequences of 5.8-S ribosomal RNA from Xenopus laevis  
 and Xenopus borealis  
 EUR. J. BIOCHEM. 87 (1), 199-214 (1978)  
 JOURNAL MEDLINE 78214616  
 PUBMED 666689  
 COMMENT This sequence was assembled from refs. 1-6 above. The rRNA gene is  
 present as multiple tandem repeats. The non-transcribed region is  
 approximately 5Kb long, and includes entries XLRN03 and XLRN06.  
 There is considerable variation between gene copies in all the  
 non-coding regions, as described in 1-7 and references therein.  
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 intron 317..1029  
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 rRNA 1030..2854  
 /product="18S ribosomal RNA"  
 intron 2855..3411  
 /note="internal transcribed spacer 1"  
 rRNA 3412..3573  
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 rRNA 3836..7917  
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 Matches 152; Conservative 0; Mismatches 148;  
 Cy 23 GCGAAGTGGGGCGGGCGGCTGCGGAGACAAAGCGGGCGGCTGCTTCACA 82  
 Db 3012 GCGAGGGGGGGGGGGGGGGGGCGGGGTCACCCCGGGCGGCTGCTCCCGCGC 3071  
 Cy 83 GGGGCCGAGCGCTGCGCAAGAGAGAGTCTTCAGAGCGCGGAGAGGAGGCGACGGGC 142  
 Db 3072 GGGCGCGCGCGGGTACTGACCG-GGGCGGGGGCGGGGGGCTGGCGCGGAGCGGGCGG 3130  
 Cy 143 TTCCCGAGGGCGCGCGCGGACAGAGAGTTCGCGAGGCGACGGCGGTGAGCGGAGCGG 202

Db 3131 GCCCAGAGGCGCTCCGCTCCCGGCTCCGCTCCCGGAGACCCCGCGCGGTTGCA 3190  
Qy 203 GCAGAGCTTCTCAGAGAGCGCGGCGAGCGCGCTGAGAGGCGAGAGCCGGGTATTA 262  
Db 3191 AGACCCCG 3250  
Qy 263 GAAGCCCTCTGAGCTTCCCGCGAGCGCGAGGTTCCCGCGCGCGCGCGCGCGCGCGCG 322  
Db 3251 GCGCGCGCGCGAGCG 3310  
Qy 323 C 323  
Db 3311 C 3311

RESULT 32  
LOCUS AC100946/c 52390 bp DNA linear HTG 23-NOV-2001  
DEFINITION Mus musculus clone RP23-73E24, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC100946 GI:17059720  
VERSION AC100946.1  
KEYWORDS HTG; HTGS PHASEO.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
Brenner, S., Barina, N., Baatien, V., Boguslavsky, L., Bouckigatier, B.,  
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,  
Coke, P., Colangelo, M., Collins, S., Collymore, A., Cook, A.,  
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gaidyna, N.,  
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Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,  
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,  
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
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Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
Zaitoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE  
JOURNAL  
COMMENT  
DIRECT SUBMISSION  
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
Project Information  
Center project name: L14623  
Center clone name: 73\_E\_24

\* NOTE: This record contains 66 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for

\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
1 699: contig of 699 bp in length  
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800 1483: contig of 684 bp in length  
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3999 4698: contig of 703 bp in length  
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5000 4995: contig of 698 bp in length  
5001 5595: gap of 100 bp  
5596 5995: contig of 694 bp in length  
5996 6399: gap of 100 bp  
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25430 26120: contig of 690 bp in length  
26121 26220: gap of 100 bp  
26221 26911: contig of 692 bp in length



TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Olarnpunasagoon, A., Pal, S., Parke, K., Pasternak, S., Paul, H.,  
Perez, A., Perez, L., Frankoch, C., Plopper, F., Poidexter, A.,  
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Holt, R. A., Smith, H. O., Weinstein, G. and Gibbs, R. A.

Unpublished  
2 (bases 1 to 123865)  
Direct Submission  
Submitted (12-APR-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
Project Information  
Center Project name: GWAT  
Center Clone name: CH230-111P8  
Summary Statistics  
Sequencing Vector: Plasmid;  
Chemistry: Dye-terminator Big Dye 1004 of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 99629 bases at least Q40  
Consensus quality: 110813 bases at least Q30  
Consensus quality: 119224 bases at least Q20  
Quality coverage: 0x in Q20 bases; sum-of-coverage estimation

NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
NOTE: This is a 'working draft' sequence. It currently  
consists of 65 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.  
This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.

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[illegible]

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----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-terminator BigDye; 100% of reads
Assembly program: Phrap; version 0.990119
Consensus quality: 205914 bases at least Q40
Consensus quality: 206414 bases at least Q40
Consensus quality: 206846 bases at least Q20
Insert size: 16800; agarose-fp
Insert coverage: 20.39 in Q20 bases; sum-of-contigs
Quality coverage: 11.34 in Q20 bases; sum-of-contigs
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NOTE: This is a "working draft" sequence. It currently
consists of 6 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

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      *     1       3490: gap of unknown length
      *     2       3491       8170: contig of 4680 bp in length
      *     3       8171       8270: gap of unknown length
      *     4       8271       45642: contig of 37372 bp in length
      *     5       45643       82012: gap of unknown length
      *     6       82012       82112: contig of 36270 bp in length
      *     7       82113       82113: gap of unknown length
      *     8       82113       143988: contig of 61886 bp in length
      *     9       143989       144098: gap of unknown length
      *    10       144099       209257: contig of 65159 bp in length.

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Location/Qualifiers
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Best Local Similarity 51.7%; Pred.No.1.6;
Matches 169; Conservative 0; Mismatched 153; Indels 5; Gaps 2;

OY        1         GCCGCTGGAGTCAACCGCAAAGCAGAATGCCGCAGGTGGCCCTTCGCCGAACAATAA 60
Db         143821  GCACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 143762
OY        61        GGCGCGCGCTTGACTTTCTTAAGAGGC----CCAAGCGCTTGCCAAAGAGAATTCTTAGAG 116
Db         143761  GCACGCGGTTCGAGCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 143702
OY        117       GCCCGGAGGAGGAAGGAGGACATGAGCTTCCAGAGACCACGCGCGCGCGCACAGAGGAATTGG 176
Db         143701  CGCGGAGGAGGCGCATGAGGCGCGGAGGCGGAGCGGAGCGGAGCGATCCGAGCGCCGCGCGCGG 143642
OY        177       CCAAGGCAAGCGCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 236
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[illegible][illegible]

RESULT	35				
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LOCUS	AB053222				
DEFINITION	Homo sapiens gene for N-acetylglucosaminyltransferase IVa, partial				
NITRONTN					
		12662 bp	DNA	linear	PRI_08-JAN-2003
AB053222					

ACCESSION VERSION KEYWORDS SOURCE	AB053222 AB053222.1	GI:27544617
	Homo sapiens (human)	

REFERENCE	AUTHORS	TITLE
1	Minowa, M. T. and Takeuchi, M.	Alternative splicing in human N-acetylglucosaminyltransferase IVa

Unpublished  
2 (bases 1 to 12562)  
Minowa, M. T. and Yoshida, A.  
Direct Submission  
Submitted (05-JAN-2001) Aruco Yoshida, Central Labs. for Key  
Technology, Kirin Brewery Co., Ltd.; Kanazawa-ku, Fuku-ura, 1-13-5-  
Yokohama, Kanagawa 236-0004, Japan (E-mail: ayoshida@kirin.co.jp,  
Tel: 81-45-788-7361, Fax: 81-45-788-4042)

FEATURES	Location/Qualifiers
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	"where source"

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/mol_type="genomic DNA"
/db_xref="taxon:9606"
5595. 5636
exon

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exon	10116..10444
note="alternative splicing exon' or exon2"	
evidence=experimental	
CDS	10351..>10444

BASE COUNT	3336	a	2531	c	3005	g	3676	t	14	others
ORIGIN	/translatation="MRLNGTVAATATAFITSFLTITSWYTTWONGK"									

	Query Match	16.1%;	Score 52;	DB 9;	Length 12562;
	Best Local Similarity	48.1%;	Pred. No. 3.2;		
	Matches 155;	Conservative	0;	Mismatches 155;	Indels 0;
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QY	74	TCTCTAAGAGGCGCCCGACGGCGCTGCACAAAGGAATCTTCAGGGCCCGGCGAGGAAAGG	133		
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QY	134	GGCAGCGGCTTCCCAAGGCGCCGCGCGCGCCGACACAGAAATTGCCAGGAGCAACGGCGCTGGA	193		
Db	5579	GGGGGCGGCTACACAGACTCTCCGCGGGCAGCCGGGAGACGAGCCGACCTCAGCGCGGT	5638		

**RESULT** 36  
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**LOCUS** Homo sapiens BAC clone Rpl1-764Ds from 2, complete sequence.  
**DEFINITION** ACI09826 AC061962  
**ACCESSION** ACI09826.4 GI:27905024  
**VERSION** HTG.  
**KEYWORDS** Homo sapiens (human)  
**SOURCE** Homo sapiens  
**ORGANISM** Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

REFERENCE	1 (bases 1 to 87746)
AUTHORS	Sulston, J.E. and Waterston, R.
TITLE	Toward a complete human genome sequence
JOURNAL	Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE	93063792
PUBMED	9847074
REFERENCE	2 (bases 1 to 87746)
AUTHORS	Tomlinson, C., Meyer, R. and Dignam, G.
TITLE	The sequence of Homo sapiens BAC clone RP11-764D5
JOURNAL	Unpublished (2001)
REFERENCE	3 (bases 1 to 87746)
AUTHORS	Waterston, R.H.
TITLE	Direct Submission
JOURNAL	Submitted (07-FEB-2002) Genome Sequencing Center, Washington

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

MO 63106, USA  
4 (bases 1 to 87746)  
Waterston, R.H.  
Direct Submission  
Submitted (11-MAR-2002) Genome Sequencing Center, Washington  
444 Woodruff Park Parkway St Louis

REFERENCE	5 (bases 1 to 87746)
AUTHORS	Waterston, R.
TITLE	Direct Submission
JOURNAL	Submitted (27-NOV-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE	6 (bases 1 to 87746)
AUTHORS	Waterston, R.

**JOURNAL** Submitted (27-JAN-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
**COMMENT** On Jan 27, 2003 this sequence version replaced gi:25777545.

Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc>  
Contact: [saplens@watscn.wustl.edu](mailto:saplens@watscn.wustl.edu)  
----- Summary Statistics -----  
Center project name: H\_NH0764D05  
Drafting Center: WIBR

NOTE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring data submissions.



QY 74 TCTCTAGAGGGGCCCCAGCGCCCTCCAGAGAGATCTCTGAGAGCCCGGCGAGAGAGG 133  
 Db 24102 AGCGGGGGGGGGCGAGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 24043  
 QY 134 GGCACGCGGCTTCCAGAGGGCCCGCGCGCGAGAGAGAGTTGGCCAGGGGACCGGCTTGA 193  
 Db 24042 GCGCGGGGCTTACAGCAGCTCCCGCGAGCGCGAGAGAGAGCGGAGAGCGGAGCGGT 23983  
 QY 194 GCGAGAGCGGCGAGGCGCTTCTCAGAGAGCGGCGAGAGCGCGCGCTTGAAGGCGAGAC 253  
 Db 23982 GAGGGGCTCCGCGCGAGCGCGCGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGG 23923  
 QY 254 CCGGATATAGAGCGCTCTGAGCGCTTGGCCCGGAGCGCGAGTTTCCCGCGCGCGGAG 313  
 Db 23922 CGGAGCGCGGGGAGTTGGGGGGCGCGCGCGCGCGCGCGCGCTGCGCGCGCTCGG 23863

RESULT 37  
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 DEFINITION  
 AC105035  
 AC105035  
 VERSION HTG: HTG\_PHRASED  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 67246)  
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 Homo sapiens chromosome 8, clone CTD-230711  
 Unpublished  
 2 (bases 1 to 67246)  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,  
 Anderson, S., Barina, N., Baastien, V., Boguslavsky, L., Boukhalter, B.,  
 Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,  
 Choquel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,  
 Cooke, P., DeArrelano, K., Dewar, K., Diaz, J. S., Dodge, S., Fato, S.,  
 Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, N.,  
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,  
 Hages, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,  
 Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K.,  
 Lamazares, R., Landers, T., Lehotzky, J., Levine, R., Liu, G.,  
 Maclean, C., Macdonald, P., Major, J., Marguis, N., Matthews, C.,  
 McCarthy, M., McEwan, P., McKernan, K., McPherson, R., Melidoni, J.,  
 Mensen, L., Mihova, T., Mienna, V., Murphy, T., Naylor, J., Nguyen, C.,  
 Oliver, C., Norman, C. H., O'Donnell, P., O'Neill, D.,  
 O'Neill, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,  
 Raymond, C., Rietz, M., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
 Roman, S., Sevel, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
 Strauss, N., Subramanian, A., Talamas, J., Testafay, S., Theodore, J.,  
 Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,  
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, M. J., Young, G.,  
 Zaitoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE  
 JOURNAL  
 COMMENT  
 Direct Submission  
 Submitted (22-DEC-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 All repeats were identified using RepeatMasker:  
 Smith, A. F. A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RW/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 Project Information  
 Center project name: L23018  
 Center clone name: 2307\_I\_1

\* NOTE: This record contains 82 individual

\* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
 \* be preserved.  
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 \* 11333: contig of 710 bp in length  
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 \* 24429: gap of 100 bp  
 \* 24429: contig of 727 bp in length  
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 \* 25254: contig of 727 bp in length  
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* 26191 26190: contig of 729 bp in length
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* 27020 27019: contig of 726 bp in length
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* 27846 27845: contig of 714 bp in length
* 28560 28659: gap of 100 bp
* 28660 28659: contig of 712 bp in length
* 29372 29471: gap of 100 bp
* 29472 29471: contig of 705 bp in length
* 30177 30276: gap of 100 bp
* 30277 30276: contig of 736 bp in length
* 31013 31112: gap of 100 bp
* 31113 31137: contig of 725 bp in length
* 31838 31937: gap of 100 bp
* 31938 32600: contig of 663 bp in length
* 32601 32700: gap of 100 bp
* 32701 33430: contig of 730 bp in length
* 33431 33530: gap of 100 bp
* 33531 34355: contig of 725 bp in length
* 34356 35092: contig of 737 bp in length
* 35093 35192: gap of 100 bp
* 35193 35900: contig of 708 bp in length
* 35901 36000: gap of 100 bp
* 36001 36715: contig of 715 bp in length
* 36716 37526: contig of 711 bp in length
* 37527 37626: gap of 100 bp
* 37627 38344: contig of 718 bp in length
* 38345 38444: gap of 100 bp
* 38445 39282: contig of 738 bp in length
* 39283 40016: gap of 100 bp
* 40017 40850: contig of 734 bp in length
* 40851 40950: gap of 100 bp
* 40951 41640: contig of 690 bp in length
* 41641 41740: gap of 100 bp
* 41741 42472: contig of 732 bp in length
* 42473 42572: gap of 100 bp
* 42573 43300: contig of 728 bp in length
* 43301 43400: gap of 100 bp
* 43401 44126: contig of 726 bp in length
* 44127 44226: gap of 100 bp
* 44227 44913: contig of 687 bp in length
* 44914 45013: gap of 100 bp
* 45014 45719: contig of 706 bp in length
* 45720 46534: contig of 715 bp in length
* 46535 47353: gap of 100 bp
* 47354 47453: contig of 718 bp in length
* 47454 48187: gap of 100 bp
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* 48288 49016: gap of 100 bp
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* 50689 50769: contig of 715 bp in length
* 50770 51511: gap of 100 bp
* 51512 51612: contig of 742 bp in length
* 51613 52338: gap of 100 bp
* 52339 52438: contig of 727 bp in length
* 52439 53172: gap of 100 bp
* 53173 53272: contig of 734 bp in length
* 53273 54007: gap of 100 bp
* 54008 54107: contig of 735 bp in length
* 54108 54809: gap of 100 bp
* 54810 54909: contig of 702 bp in length
* 55614 55714: gap of 100 bp

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* 55715 56431: contig of 717 bp in length
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Best Local Similarity 50.4%; Pred. No. 2.4;
Matches 125; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

1 GCGCGTGGGCGCAGACCCGCAAGCGAAGTGGCGGGCGGGGGGCTTCGCGAGCANA 60
11329 GGGGGGGGGGAGAGGGGAGAGAGCGCGCGGGCGGGGGGGGGGGGGGGGGGGGGGG
Db GGGGGGGGGGAGAGGGGAGAGAGCGCGCGGGCGGGGGGGGGGGGGGGGGGGGGGG
Qy 61 GCGCGGCGCTTCCTCTCTCAAGAGGGGCCCGCGCTTCGCAAGAGAGTCTTCGAGCGCC 120
11269 GCGGGCGGGGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Db 121 GCGCGAGGAGAGGGGGGGCGAGGGCTTCGAGAGCGCGCGCGCGAGAGAGAGTGGCGCAG 180
11209 GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Qy 181 GCGCAGGCGCGTCAAGCGAGCGGGCGGGCTTTCGAGAGCGCGGGCGAGAGGGCGCTG 240
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Db 241 GAGGGGCGG 248
Qy 11089 GGGGGGGGG 11082
Db

RESULT 38
AC084084
LOCUS
DEFINITION
AC084084 Homo sapiens chromosome 8 clone RP11-314C19 map 8, LOW-PASS
SEQUENCE SAMPLING.
AC084084 AC084084.2 GI:13446278
VERSION
HTG; HTGS PHASE0.
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 71032)
REFERENCE
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, clone RP11-314C19
unpublished
2 (bases 1 to 71032)
REFERENCE
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavsky, L.,
Boukhalil, B., Brown, A., Burkett, G., Campoliano, A., Castele, A.,
Chokgel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Darell, K., Dewar, K., Diaz, J. S., Dodge, S., Ferreira, P.,
Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,
Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L.,
Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Larocque, K.,
Lima, R., Lander, E., Lewis, T., Levine, R., Liu, G.,
Macdonald, P., Margulis, N., McCarthy, M., McEwan, P., McKernan, K.,
McPheters, R., Meidirim, U., Menais, L., Mihova, T., Mleaga, V.,
Morrow, U., Murphy, T., Naylor, U., Norman, C. H., O'Connor, T.,
O'Donnell, P., O'Neill, D., Oliveira, T. M., Oliver, J., Peterson, K.,
Pierce, N., Pisanu, C., Pollara, V., Raymond, C., Rieback, M., Riley, R.,
Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,
Sougnuez, C., Spencer, B., Stange, T., Thomas, N., Stojanovic, N.,
Straus, N., Subramanian, A., Talamas, U., Testa, S., Theodore, J.,
Tirrell, A., Travers, M., Triggillo, U., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. D., Young, G., Zaitoun, J.,
Zimmer, A. and Zody, M.
Direct Submission
Submitted (12-OCT-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 25, 2001 this sequence version replaced gi:10799449.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research

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Center code: WIBR  
Web site: http://www.seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
Project Information  
Center project name: L1327  
Center clone name: 314\_C\_19

NOTE: This record contains 85 individual  
sequencing reads that have not been assembled into  
contigs. Runs of N are used to separate the reads  
and the order in which they appear is completely  
arbitrary. Low-pass sequence sampling is useful for  
identifying clones that may be gene-rich and allows  
overlap relationships among clones to be deduced.  
However, it should not be assumed that this clone  
will be sequenced to completion. In the event that  
the record is updated, the accession number will  
be preserved.

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5916 6648: contig of 733 bp in length  
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6749 7520: contig of 772 bp in length  
7521 8347: contig of 727 bp in length  
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16003 16712: contig of 710 bp in length  
16713 16811: gap of 100 bp  
16812 17539: contig of 728 bp in length  
17540 17639: gap of 100 bp  
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19163 19262: gap of 100 bp  
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Fri Nov 7 08:10:01 2003

us-10-081-817a-19\_copy\_229\_551.rge

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Qy	247	CGAGGACCGGGTAAAGAGCCTCGTGGCCTTGCCCGGCAAGCCGAGGTTCCCGCGG	306
Db	716	CGCGGGGGCGCGGGGGGGCGCGCGGGGGGGGGCGGGGGGGGGGGGGGGGGGG	657
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Search completed: November 6, 2003, 08:07:12  
Job time : 1962.81 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: November 6, 2003, 06:12:36 ; Search time 234.409 Seconds  
3719.648 Million cell updates/sec

Title: US-10-081-817a-19\_COPY\_229\_551

Perfect score: 323  
Sequence: 1 gcgcgtggggtcagaccgca.....gcgcgcgagcccgccgccc 323

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: N\_Geneseq\_19jun03.\*

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25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	296.8	91.9	1794	24	ABT06542 Human HIN-1 coding
2	120	37.2	19	AAVS4620	Human HIN-1 coding
3	117	36.2	19	AAVS4616	Human HIN-1 coding
4	92	28.5	21	AA298173	Human signal pepti
5	92	28.5	21	AA29723	Human lung specifi
6	78	24.1	19	AAVS4621	Human lung specifi
7	78	24.1	24	ABK40267	cdna encoding huma
8	78	24.1	21	AA265103	Membrane-bound pro

#### ALIGNMENTS

RESULT 1	ID	ABT06542	standard; DNA; 1794 BP.
XX	AC	ABT06542;	
XX	DT	07-NOV-2002 (first entry)	
XX	DE	Human HIN-1 coding sequence.	
XX	KW	Human; methylated gene; breast cancer; marker; WT-1;	
XX	KW	cell proliferative disorder; TWIST; HOKAS; NES-1; RABbeta; cyclin D2;	
XX	KW	retinoid acid receptor beta; oestrogen receptor; Wilms' tumour;	
XX	KW	14.3.3 sigma; HIN-1; RASST1a; tumour suppressor gene; hypermethylation;	
XX	OS	gene; promoter; ds.	
XX	OS	Homo sapiens.	
XX	FN	WO200259347-A2.	
XX	PD	01-AUG-2002.	
XX	PF	28-JAN-2002; 2002WO-US02455.	
XX	PR	26-JAN-2001; 2001US-0771357.	
XX	PA	(UYUO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.	
XX	PI	Sukumar S, Evron E, Doolley WC, Sacchi N, Davidson N, Packler MJ;	
XX	XX	WPI; 2002-599803/64.	

XX Diagnosing and/or determining a predisposition to a cellular  
 PT proliferative disorder of breast tissue, in particular breast cancer,  
 PT by determining the state of methylation of one or more nucleic acids  
 PT isolated from the subject  
 PS  
 XX Disclosure; Fig 9A; 115p; English.  
 XX  
 CC The present invention relates to a method of diagnosing a cellular  
 CC proliferative disorder of breast tissue, which involves determining the  
 CC state of methylation of one or more nucleic acids isolated from the  
 CC subject, where the state of methylation of the nucleic acids as compared  
 CC with a state of methylation from a subject not having the cellular  
 CC proliferative disorder of breast tissue is indicative of a cellular  
 CC proliferative disorder of breast tissue in the subject. The nucleic acids  
 CC may be TWIST, HoxA5, NES-1, retinoic acid receptor beta (RARbeta),  
 CC oestrogen receptor, cyclin D2, Wilm's tumour gene (WT-1), 14.3.3 sigma,  
 CC HIN-1 or RASBP1A. The method is useful for diagnosing and/or determining  
 CC a predisposition to a cellular proliferative disorder, in particular  
 CC breast cancer including ductal carcinoma in situ, lobular carcinoma,  
 CC colloid carcinoma, tubular carcinoma, medullary carcinoma, metaplastic  
 CC carcinoma, intraductal carcinoma in situ, lobular carcinoma in situ and  
 CC papillary carcinoma in situ. The present sequence is a gene fragment used  
 CC in the exemplification of the invention.  
 CC  
 XX Sequence 1794 BP; 240 A; 646 C; 522 G; 318 T; 68 other;

Query Match 91.9%; Score 296.8; DB 24; Length 1794;

Best Local Similarity 93.7%; Pred. No. 8.5e-53;

Matches 288; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 6 TGGGCTCAGACCCCAAGCGAGCTCGCGGCTGCGCTCTCGCGAGACAAAGCCG 65  
 DB 854 TGGGGTCAACCGCAAGCGAGCTCGCGGCTGCGCTCTCGCGAGACAAAGCCG 913  
 QY 66 GGCCTCCTCTCTCAGAGGGCCCGCAGCGCTGCGCAAGAGATCTCTCAGAGCCCGGCA 125  
 DB 914 GGCCTCCTCTCTCAGAGGGCCCGCAGCGCTGCGCAAGAGATCTCTCAGAGCCCGGCA 973  
 QY 126 GGGAGGGGGCAAGGGGCTTCCAGGGCCCGCGCGCGAGAGAGTGGCCAGGGGCA 185  
 DB 974 GGGAGGGGGCAAGGGGCTTCCAGGGCCCGCGCGCGAGAGAGTGGCCAGGGGCA 1033  
 QY 186 GGGCGGAGCGAGCGAGGGGCTTCTCAGAGGGCGGGGAGGGCGCGCTGAGAGG 245  
 DB 1034 GGGCGGAGCGAGCGAGGGGCTTCTCAGAGGGCGGGGAGGGCGCGCTGAGAGG 1093  
 QY 246 GCGAGAGCGCGGCTATAGAGCTGAGCTTGCCTGCGCGAGCGCGAGTCCCGGGG 305  
 DB 1094 GNN 1153  
 QY 306 GCGCCGAGCGCCCGCGCCG 323  
 DB 1154 GCGCCGAGCGCCCGCGCCG 1171

RESULT 2

AAVS4620  
 ID AAVS4620 standard; cDNA; 562 BP.

XX AAVS4620;

XX 25-MAR-2003 (updated)

XX 30-OCT-1998 (first entry)

XX LU105 specific consensus polynucleotide sequence.

XX LU105; lung disease marker; immunosassay; lung disease; cancer;

XX blood; plasma; serum; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 122..436  
 FT /tag= a  
 FT /transl\_except= (pos:176..178, aa:Val)  
 FT /product= "LU105 polypeptide"  
 XX  
 XX W09833926-A1.  
 XX  
 XX 06-AUG-1998.  
 XX  
 XX 30-JAN-1998; 98WO-US01766.  
 XX  
 XX 31-JAN-1997; 97US-0791710.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 XX  
 XX Billing-medet PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 XX Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertstrapp L;  
 XX Russell JC, Stroupe SD;  
 XX WPI: 1998-437479/37.  
 XX P-PSDB: AAW75868.  
 XX  
 XX New nucleic acid for the lung disease marker LU105 - polypeptides,  
 XX antibodies and genes, used for diagnosis, prevention, treatment of  
 XX lung disease, specifically cancer  
 XX  
 XX Claim 11; Fig 1; 123p; English.

XX Sequences shown in AAVS4616 to AAVS4621 represent LU105 specific  
 CC polynucleotide sequences. These are used in the method of the invention  
 CC for detecting target LU105 nucleic acid. The method comprises treating a  
 CC sample with at least one LU105 specific nucleic acid, or its complement  
 CC which is at least 50 percent identical with the LU105 specific nucleic  
 CC acid sequences (AAVS4616 to AAVS4621). LU105 is a lung disease marker.  
 CC Cells transfected with a recombinant expression system that contains  
 CC LU105 polypeptides which are used to raise antibodies. The antibodies are  
 CC used to detect the LU105 antigen, and correspondingly this antigen is  
 CC used to detect specific antibodies, in usual immunoassays. The LU105  
 CC polypeptides and nucleic acid sequences are used for diagnosis, staging,  
 CC monitoring, prognosis, prevention, treatment and determination of  
 CC susceptibility to, lung disease, specifically cancer. The LU105  
 CC polypeptides are also used to screen for specific binding agents, useful  
 CC therapeutically. LU105 is a marker for lung disease (present at high  
 CC concentration in altered form or in an unusual body compartment). LU105  
 CC can be detected in blood, plasma or serum in an inexpensive, non-invasive  
 CC test  
 CC  
 XX (updated on 25-MAR-2003 to correct PI field.)

Query Match 37.2%; Score 120; DB 19; Length 562;

Best Local Similarity 99.2%; Pred. No. 3.2e-16;

Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GCAAGGCTTTCTCAGAGCGCGGCGAGCCCGCGCTGAGAGGGCGAGAGACCGGGTATTA 262  
 DB 1 GCAAGGCTTTCTCAGAGCGCGGCGAGCCCGCGCTGAGAGGGCGAGAGACCGGGTATTA 60  
 QY 263 GAAAGCTCTGAGCTTCCCGGCGAGCCCGAGATTCCCGCGCGCCCGAGCCCGCGCGC 322  
 DB 61 GAAAGCTCTGAGCTTCCCGGCGAGCCCGAGATTCCCGCGCGCCCGAGCCCGCGCGC 120  
 QY 323 C 323  
 DB 121 C 121

RESULT 3

AAVS4616  
 ID AAVS4616 standard; cDNA; 190 BP.

XX AAVS4616;

XX 25-MAR-2003 (updated)  
 DT 30-OCT-1998 (first entry)  
 XX  
 DE LUI05 specific polynucleotide sequence from clone 3353867.  
 XX  
 KW LUI05; lung disease marker; immunoassay; lung disease; cancer;  
 KM blood; plasma; serum; ss.  
 XX Homo sapiens.  
 XX MO9833926-A1.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PF 30-JAN-1998; 98WO-US01766.  
 XX  
 PR 31-JAN-1997; 97US-0791710.  
 XX  
 PA (ABBO) ABBOTT LAB.  
 XX  
 PI Billing-medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Grandos EN, Hodges SC, Klass MR, Kratochvil JD, Robertstrapp L;  
 PI Russell JC, Strophe SD;  
 XX WPI; 1998-437479/37.  
 DR  
 XX New nucleic acid for the lung disease marker LUI05 - polypeptides,  
 PI antibodies and genes, used for diagnosis, prevention, treatment of  
 PI lung disease, specifically cancer  
 XX  
 PS Claim 11; Fig 1; 123pp; English.  
 CC Sequences shown in AAV54616 to AAV54621 represent LUI05 specific  
 CC polynucleotide sequences. These are used in the method of the invention  
 CC for detecting target LUI05 nucleic acid. The method comprises treating a  
 CC sample with at least one LUI05 specific nucleic acid, or its complement  
 CC which is at least 50 percent identical with the LUI05 specific nucleic  
 CC acid sequences (AAV54616 to AAV54621). LUI05 is a lung disease marker.  
 CC Cells transformed with a recombinant expression system that contains  
 CC LUI05 specific nucleic acid fragments, are used to express recombinant  
 CC LUI05 polypeptides which are used to raise antibodies. The antibodies are  
 CC used to detect the LUI05 antigen, and correspondingly this antigen is  
 CC polypeptides and nucleic acid sequences are used for diagnosis, staging,  
 CC monitoring, prognosis, prevention, treatment and determination of  
 CC susceptibility to, lung disease, specifically cancer. The LUI05  
 CC polypeptides are also used to screen for specific binding agents, useful  
 CC therapeutically. LUI05 is a marker for lung disease (present at high  
 CC concentration, in altered form or in an unusual body compartment). LUI05  
 CC can be detected in blood, plasma or serum in an inexpensive, non-invasive  
 CC test.  
 CC (updated on 25-MAR-2003 to correct PI field.)  
 CC  
 SO Sequence 190 BP; 18 A; 69 C; 67 G; 32 T; 4 other;  
 Query Match 36.2%; Score 117; DB 19; Length 190;  
 Best Local Similarity 96.7%; Pred. No. 1,4e-15;  
 Matches 117; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 203 GCGAGGCTTTCTAGAGAGCGCGGCGAGCGCGCTGAGAGGCGAGAGCGCGGTATTA 262  
 DB 1 GCGAGGCTTTCTAGAGAGCGCGGCGAGCGCGCTGAGAGGCGAGAGCGCGGTATTA 60  
 QY 263 GAAGCTCTGCTGCTGCGCGGCGAGCGCGAGGTTCCCGCGCGCGCCGAGCGCGCGGC 322  
 DB 61 GAAGCTCTGCTGCTGCGCGGCGAGCGCGAGGTTCCCGCGCGCGCCGAGCGCGCGGC 120  
 QY 323 C 323  
 DB 121 C 121

RESULT 4  
 ID AA298173 standard; CDNA; 543 BP.  
 XX  
 AC AA298173;  
 XX  
 DT 11-MAY-2000 (first entry)  
 XX  
 DE Human signal peptide containing protein HSP-65 CDNA SEQ ID NO:199.  
 XX  
 KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;  
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
 KW antimicrobial; neuroprotective; cardiovascular; hepatocytic;  
 KW antiaesthetic; gene therapy; cell proliferation; neurological disorder;  
 KW reproductive disorder; developmental disorder; arteriosclerosis;  
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anemia;  
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
 KW Parkinson's disease; Huntington's disease; ovulatory defect;  
 KW muscular dystrophy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200000610-A2.  
 XX  
 PD 06-JAN-2000.  
 XX  
 PF 25-JUN-1999; 99WO-US14484.  
 XX  
 PR 26-JUN-1998; 98US-0090762.  
 XX  
 PR 31-JUL-1998; 98US-0094983.  
 XX  
 PR 01-OCT-1998; 98US-0102686.  
 XX  
 PR 11-DEC-1998; 98US-0112129.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn ME;  
 PI Akerbloom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
 PI Bandman O;  
 XX WPI; 2000-160673/14.  
 DR P-PSDB; AAY87288.  
 XX  
 PT New human signal peptide-containing proteins useful in treatment,  
 PT prevention and diagnosis of e.g. cancer, inflammation and  
 PT cardiovascular disease  
 XX  
 PS Claim 9; Page 289; 327pp; English.  
 CC AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the  
 CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have  
 CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,  
 CC neuroprotective, cardiovascular and antiaesthetic activities, and can  
 CC be used in gene therapy. HSPs can be used to treat or prevent disorders  
 CC associated with decreased activity or function of HSP. Antagonists of  
 CC HSP are used to treat or prevent disorders associated with increased  
 CC activity or function of HSP. Such diseases include cell proliferation  
 CC (including cancer), inflammation, cardiovascular, neurological,  
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anemia, or  
 CC asthma, Crohn's disease, Alzheimer's, Parkinson's or Huntington's  
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP  
 CC nucleic acids can be used for the recombinant production of HSP, for  
 CC detecting HSP in standard hybridisation and amplification assays (for  
 CC diagnosis and monitoring), in gene therapy, as antisense,  
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences  
 CC or genetic variations, and for chromosomal mapping. HSP are also used to  
 CC raise specific antibodies (Ab) and to screen for agonists and  
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or  
 CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic  
 CC antagonists, in competitive drug screens, and for purification of HSP  
 CC from natural sources.

SQ Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 other;

Query Match 28.5%; Score 92; DB 21; Length 543;  
Best Local Similarity 100.0%; Pred. No. 2e-10;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 CCGGCGCTGGAGGCGGAGACCGGGTATTAAGAGCTTCGTGCGCTTGGCCGGGACGCCG 291  
DB 1 CCGGCGCTGGAGGCGGAGACCGGGTATTAAGAGCTTCGTGCGCTTGGCCGGGACGCCG 60

QY 292 CAGGTTCCCGCGCGCGCGCGAGCCCGCGCGCC 323  
DB 61 CAGGTTCCCGCGCGCGCGCGAGCCCGCGCGCC 92

RESULT 5

AA229723 standard; DNA; 543 BP.

AA229723;

27-MAR-2000 (first entry)

Human lung specific gene lng107.

Lung Specific Gene; LSG; lng107; human; diagnostic marker;

prognosticate; lung cancer; diagnosis; ds.

Homo sapiens.

Location/Qualifiers

Key 93.407  
CDS /tag= a  
/product= "LSG lng107 protein"

MO960160-A1.

25-NOV-1999.

12-MAY-1999; 99WO-US10344.

21-MAY-1998; 98US-0086212.

(DIAD-) DIADEXUS LLC.

Yang F, Macina RA, Sun Y;

WPI; 2000-116320/10.

P-PSDB; AAY44458.

A new method for diagnosing, monitoring and staging lung cancer -

Claim 6; Page 36; 40pp; English.

The present sequence is a lung specific gene (LSG) lng107 from human  
clone ID 562271. The LSG has high level of tissue specificity for lungs  
and is overexpressed in cancerous tissues. The sequence serves as a  
diagnostic marker for detecting, monitoring, staging and prognosticating  
lung cancer. The diagnosis involves comparing levels of LSG in samples  
obtained from patient and normal control.

Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 other;

Query Match 28.5%; Score 92; DB 21; Length 543;  
Best Local Similarity 100.0%; Pred. No. 2e-10;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 CCGGCGCTGGAGGCGGAGACCGGGTATTAAGAGCTTCGTGCGCTTGGCCGGGACGCCG 291  
DB 1 CCGGCGCTGGAGGCGGAGACCGGGTATTAAGAGCTTCGTGCGCTTGGCCGGGACGCCG 60

QY 292 CAGGTTCCCGCGCGCGCGCGAGCCCGCGCGCC 323

DB 61 CAGGTTCCCGCGCGCGCGCGAGCCCGCGCGCC 92

RESULT 6  
AAV54621 standard; cDNA; 519 BP.

AAV54621;

25-MAR-2003 (updated)

30-OCT-1998 (first entry)

LJ105 polypeptide encoding cDNA clone 13278361H.

LJ105; lung disease marker; immunoassay; lung disease; cancer;

blood; plasma; serum; ss.

Homo sapiens.

Location/Qualifiers

Key 79.393  
CDS /tag= a  
/transl\_except= (pos:136..138, aa:Val)  
/product= "LJ105 polypeptide"

WO9833926-A1.

06-AUG-1998.

30-JAN-1998; 98WO-US01766.

31-JAN-1997; 97US-0791710.

(ABBO) ABBOTT LAB.

Billing-medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;

Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertstrapp L;

Russell JC, Stroupe SD;

WPI; 1998-437479/37.

P-PSDB; AAW75868.

New nucleic acid for the lung disease marker LJ105 - polypeptides,

antibodies and genes, used for diagnosis, prevention, treatment of

lung disease, specifically cancer

Claim 11; Fig 1; 123pp; English.

Sequences shown in AAV54616 to AAV54621 represent LJ105 specific  
polynucleotide sequences. These are used in the method of the invention  
for detecting target LJ105 nucleic acid. The method comprises treating a  
sample with at least one LJ105 specific nucleic acid, or its complement  
which is at least 50 percent identical with the LJ105 specific nucleic  
acid sequences (AAV54616 to AAV54621). LJ105 is a lung disease marker.  
Cells transformed with a recombinant expression system that contains  
LJ105 specific nucleic acid fragments, are used to express recombinant  
LJ105 polypeptides which are used to raise antibodies. The antibodies are  
used to detect the LJ105 antigen, and correspondingly this antigen is  
used to detect specific antibodies in usual immunoassays. The LJ105  
polypeptides and nucleic acid sequences are used for diagnosis, staging,  
monitoring, prognosis, prevention, treatment and determination of

susceptibility to, lung disease, specifically cancer. The LJ105  
polypeptides are also used to screen for specific binding agents, useful  
therapeutically. LJ105 is a marker for lung disease (present at high  
concentration, in altered form or in an unusual body compartment). LJ105  
can be detected in blood, plasma or serum in an inexpensive, non-invasive  
test.

(Updated on 25-MAR-2003 to correct PI field.)

Sequence 519 BP; 78 A; 190 C; 170 G; 81 T; 0 other;

Query Match 24.1%; Score 78; DB 19; Length 519;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;

QY 519 CAGGTTCCCGCGCGCGCGCGAGCCCGCGCGCC 323

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GCGAGACCGGGATTAAGAGCCTTGCTGCTTCCCGGAGACCCGAGGTTCCCGGCC 305  
 Db 1 GCGAGACCGGGATTAAGAGCCTTGCTGCTTCCCGGAGACCCGAGGTTCCCGGCC 60

QY 306 GCGCCGAGCCCGCGGCC 323  
 Db 61 GCGCCGAGCCCGCGGCC 78

RESULT 7  
 ABK40267  
 ID ABK40267 standard; cDNA; 569 BP.  
 XX  
 AC ABK40267;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE cDNA encoding human PRO1245 polypeptide.  
 XX  
 KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;  
 KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;  
 KW inflammatory disorder; immune disorder; angiogenic disorder;  
 KW gene therapy; cyostatic; neuroprotective; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200153486-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 11-FEB-2000; 2000WO-US03565.  
 XX  
 XX 08-MAR-1999; 99WO-US05028.  
 PR 11-MAR-1999; 99US-123972P.  
 PR 11-MAY-1999; 99US-133459P.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 22-JUN-1999; 99US-140650P.  
 PR 22-JUN-1999; 99US-140653P.  
 PR 20-JUL-1999; 99US-144758P.  
 PR 26-JUL-1999; 99US-145698P.  
 PR 28-JUL-1999; 99US-146222P.  
 PR 17-AUG-1999; 99US-149395P.  
 PR 31-AUG-1999; 99US-151689P.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 05-JAN-2000; 2000WO-US00219.  
 XX  
 XX (GERTH ) GENENTECH INC.  
 XX  
 FI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;  
 FI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;  
 FI Watanabe CK, Wood WI;  
 XX  
 DR WPI; 2002-205567/26.  
 DR P-PSDB; AAU86141.  
 XX  
 PT Thirty five nucleic acids encoding PRO polypeptides, useful for  
 PT treating benign or malignant tumours, leukaemias and lymphoid  
 PT malignancies, inflammatory, angiogenic and immunologic disorders -  
 XX  
 XX Claim 50; Fig 27; 302pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides and the polynucleotide sequences encoding them. The  
 CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are  
 CC useful for treating benign or malignant tumours (e.g renal, kidney,  
 CC bladder, breast, etc), leukaemias and lymphoid malignancies, other  
 CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,

CC macrophagal, stromal and blastocoele disorders, inflammatory, immune  
 CC and angiogenic disorders. The polynucleotide sequences are also  
 CC useful in gene therapy. ABK40254-ABK40288 encode for the human PRO  
 CC polypeptides of the invention.

SQ Sequence 569 BP; 128 A; 190 C; 170 G; 81 T; 0 other;

Query Match 24.1%; Score 78; DB 24; Length 569;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GCGAGACCGGGATTAAGAGCCTTGCTGCTTCCCGGAGACCCGAGGTTCCCGGCC 305  
 Db 1 GCGAGACCGGGATTAAGAGCCTTGCTGCTTCCCGGAGACCCGAGGTTCCCGGCC 60

QY 306 GCGCCGAGCCCGCGGCC 323  
 Db 61 GCGCCGAGCCCGCGGCC 78

RESULT 8  
 AAZ55103  
 ID AAZ55103 standard; cDNA; 570 BP.  
 XX  
 AC AAZ55103;  
 XX  
 DT 05-APR-2000 (first entry)  
 XX  
 DE Membrane-bound protein PRO1245 encoding cDNA.  
 XX  
 KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
 KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO9963088-A2.  
 XX  
 PD 09-DEC-1999.  
 XX  
 PF 02-JUN-1999; 99WO-US12252.  
 XX  
 XX 02-JUN-1998; 98US-0087607.  
 PR 02-JUN-1998; 98US-0087609.  
 PR 02-JUN-1998; 98US-0087759.  
 PR 03-JUN-1998; 98US-0087827.  
 PR 04-JUN-1998; 98US-0088021.  
 PR 04-JUN-1998; 98US-0088025.  
 PR 04-JUN-1998; 98US-0088029.  
 PR 04-JUN-1998; 98US-0088030.  
 PR 04-JUN-1998; 98US-0088033.  
 PR 04-JUN-1998; 98US-0088036.  
 PR 04-JUN-1998; 98US-0088167.  
 PR 05-JUN-1998; 98US-0088212.  
 PR 05-JUN-1998; 98US-0088217.  
 PR 09-JUN-1998; 98US-0088655.  
 PR 10-JUN-1998; 98US-0088722.  
 PR 10-JUN-1998; 98US-0088730.  
 PR 10-JUN-1998; 98US-0088734.  
 PR 10-JUN-1998; 98US-0088738.  
 PR 10-JUN-1998; 98US-0088740.  
 PR 10-JUN-1998; 98US-0088741.  
 PR 10-JUN-1998; 98US-0088742.  
 PR 10-JUN-1998; 98US-0088810.  
 PR 10-JUN-1998; 98US-0088811.  
 PR 10-JUN-1998; 98US-0088824.  
 PR 10-JUN-1998; 98US-0088825.  
 PR 10-JUN-1998; 98US-0088826.  
 PR 11-JUN-1998; 98US-0088851.  
 PR 11-JUN-1998; 98US-0088853.  
 PR 11-JUN-1998; 98US-0088863.  
 PR 11-JUN-1998; 98US-0088876.

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PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089410.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089601.
PR 17-JUN-1998; 98US-0089602.
PR 18-JUN-1998; 98US-0089607.
PR 18-JUN-1998; 98US-0089608.
PR 19-JUN-1998; 98US-0089647.
PR 19-JUN-1998; 98US-0089648.
PR 19-JUN-1998; 98US-0089652.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 22-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092472.
PR 10-JUL-1998; 98US-0092477.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095516.
PR 10-AUG-1998; 98US-0095529.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.

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PR 17-AUG-1998; 98US-0096757.
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PR 17-AUG-1998; 98US-0096773.
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PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
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XX (GETH ) GENENTECH INC.
XX
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX WPI: 2000-072883/06.
XX P-PSDB; MAY6757.
XX
XX Membrane-bound proteins and related nucleotide sequences
XX
XX
XX Claim 2; Fig 289; 822PP; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX sequences have homology with proteins including LDL receptors, TIE
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences
XX by recombinant techniques.
XX
XX Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;
XX
XX
XX Query Match 24.1%; Score 78; DB 21; Length 570;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-07;
XX Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 246 GCGAGGACCGGCTATAGAGGCTCTGCGCTTCCCGGACCCGAGTTCCCGGCC 305
XX 1 GCGAGGACCGGCTATAGAGGCTCTGCGCTTCCCGGACCCGAGTTCCCGGCC 60
XX
XX 306 GCCCGGAGCCCGCGGCC 323
XX 61 GCCCGGAGCCCGCGGCC 78
XX

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RESULT 9  
AAFA4249  
ID AAFA4249 standard; cDNA; 570 BP.  
XX  
AC AAFA4249;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human PRO1245 (UNO629) nucleotide sequence SEQ ID NO:407.  
XX  
XX Human; secreted and transmembrane protein; PRO; cytosolic;  
XX cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
XX diagnostic assay; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200073454-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 30-MAR-2000; 2000MO-US08439.  
XX  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 07-JUL-1999; 99US-0143048.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
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PR 15-SEP-1999; 99WO-US21090.  
PR 08-OCT-1999; 99WO-US21547.  
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PR 16-DEC-1999; 99WO-US30095.  
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PR 11-FEB-2000; 2000MO-US03565.  
PR 18-FEB-2000; 2000MO-US04341.  
PR 22-FEB-2000; 2000MO-US04414.  
PR 24-FEB-2000; 2000MO-US04914.  
PR 24-FEB-2000; 2000MO-US05004.  
PR 02-MAR-2000; 2000MO-US05841.  
PR 15-MAR-2000; 2000MO-US06884.  
PR 20-MAR-2000; 2000MO-US07377.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferreira N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX  
XX WPI; 2001-032160/04.  
XX P-PSDB; AAB65280.  
XX  
XX PRO polynucleotides used to produce polypeptides used to target  
XX specific molecules such as toxins, radiolabels or antibodies, to  
XX specific cells, to cause targeted cell death -  
XX  
XX Claim 2; Fig 289; 935gp; English.  
XX  
XX The present invention describes human secreted and transmembrane PRO  
XX proteins. The PRO proteins have cytosolic activity. The PRO proteins  
XX can be used for targeted delivery of bioactive molecules, such as  
XX toxins, radiolabels or antibodies, that cause cell death, PRO nucleotide  
XX sequences, and their fragments, can be used as hybridisation probes, in  
XX chromosomal and gene mapping, and in the generation of anti-sense RNA  
XX and DNA. They may also be used to produce transgenic animals which are  
XX used to develop and screen therapeutically useful reagents. The PRO

CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAFA4270 to AAFA4470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAFA4087 to AAFA4269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;  
XX  
Query Match 24.1%; Score 78; DB 22; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
CY 246 GCAGAGACGGGATTAAGAGCCTCGTGGCTTCCCGGAGCGGAGTTCCCGGCGC 305  
DB 1 GCAGAGACGGGATTAAGAGCCTCGTGGCTTCCCGGAGCGGAGTTCCCGGCGC 60  
CY 306 GCGCGAGCGCGCGCGCGCGC 323  
DB 61 GCGCGAGCGCGCGCGCGC 78  
XX  
RESULT 10  
ABX80386  
ID ABX80386 standard; DNA; 570 BP.  
XX  
AC ABX80386;  
XX  
DT 28-APR-2003 (first entry)  
XX  
DE Novel human secreted or transmembrane protein PRO1358 DNA.  
XX  
XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
XX cardiac insufficiency disorder; cancer; tumour; immune response;  
XX adrenal cortical capillary endothelial growth; c-fos induction;  
XX vascular endothelial growth factor inhibition; VEGF inhibition;  
XX endothelial cell growth inhibitor; T-lymphocytes stimulation;  
XX retinal neurons cell survival; rod photoreceptor cell survival;  
XX rectal disorder; retinitis pigmentosa; kidney disorder;  
XX mammalian kidney mesangial cell proliferation; Berger disease;  
XX dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
XX chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
XX  
XX Homo sapiens.  
XX  
XX US2002132252-A1.  
XX  
XX 19-SEP-2002.  
XX  
XX 14-NOV-2001; 2001US-0990442.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
XX 16-SEP-1998; 98WO-US19330.  
XX 17-SEP-1998; 98WO-US19437.  
XX 07-OCT-1998; 98WO-US21141.  
XX 01-DEC-1998; 98WO-US25108.  
XX 05-JAN-1999; 99WO-US00106.  
XX 08-MAR-1999; 99WO-US05028.  
XX 02-JUN-1999; 99WO-US12252.  
XX 15-SEP-1999; 99WO-US21547.  
XX 15-SEP-1999; 99WO-US28313.  
XX 30-NOV-1999; 99WO-US28634.  
XX 01-DEC-1999; 99WO-US28634.  
XX 16-DEC-1999; 99WO-US30095.  
XX 20-DEC-1999; 99WO-US30911.  
XX 06-JAN-2000; 2000MO-US00219.  
XX 11-FEB-2000; 2000MO-US03565.  
XX 18-FEB-2000; 2000MO-US04341.  
XX 22-FEB-2000; 2000MO-US04414.  
XX 24-FEB-2000; 2000MO-US04914.  
XX 24-FEB-2000; 2000MO-US05004.

02-MAR-2000; 2000MO-US05841.  
 PR 10-MAR-2000; 2000MO-US06319.  
 PR 15-MAR-2000; 2000MO-US06884.  
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 PR 17-MAY-2000; 2000MO-US13705.  
 PR 22-MAY-2000; 2000MO-US14042.  
 PR 30-MAY-2000; 2000MO-US14941.  
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 PR 24-AUG-2000; 2000MO-US23378.  
 PR 08-NOV-2000; 2000MO-US30952.  
 PR 01-DEC-2000; 2000MO-US32678.  
 PR 28-FEB-2001; 2001MO-US17600.  
 PR 01-JUN-2001; 2001MO-US19682.  
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 PR 09-JUL-2001; 2001MO-US21735.  
 PR 16-JUN-1997; 97US-049787P.  
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 PR 12-NOV-1997; 97US-065186P.  
 PR 13-NOV-1997; 97US-065311P.  
 PR 24-NOV-1997; 98US-066770P.  
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 PR 20-MAR-1998; 98US-078910P.  
 PR 07-MAY-1998; 98US-083322P.  
 PR 28-APR-1998; 98US-084600P.  
 PR 02-JUN-1998; 98US-087106P.  
 PR 02-JUN-1998; 98US-087609P.  
 PR 02-JUN-1998; 98US-087609P.  
 PR 03-JUN-1998; 98US-087827P.  
 PR 04-JUN-1998; 98US-088021P.  
 PR 04-JUN-1998; 98US-088025P.  
 PR 04-JUN-1998; 98US-088026P.  
 PR 04-JUN-1998; 98US-088028P.  
 PR 04-JUN-1998; 98US-088029P.  
 PR 04-JUN-1998; 98US-088030P.  
 PR 04-JUN-1998; 98US-088033P.  
 PR 04-JUN-1998; 98US-088326P.  
 PR 05-JUN-1998; 98US-088617P.  
 PR 05-JUN-1998; 98US-088620P.  
 PR 05-JUN-1998; 98US-088621P.  
 PR 05-JUN-1998; 98US-088621P.  
 PR 05-JUN-1998; 98US-088655P.  
 PR 09-JUN-1998; 98US-088734P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088742P.  
 PR 10-JUN-1998; 98US-088810P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088826P.  
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 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-089105P.  
 PR 12-JUN-1998; 98US-089440P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 16-JUN-1998; 98US-089532P.  
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 PR 28-AUG-2001; 2001US-0941992.

XX (GETH ) GENENTECH INC.  
 XX PA

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AL, Kijaviri IU, Napier MA, Pan J, Paoni NF,  
 PI Roy M, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;  
 DR WPI: 2003-247083/24.  
 DR P-PSDB; ABUS9174.  
 XX  
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1346  
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT are therapeutically useful for enhancing immune response and in cancer  
 PT treatments -  
 XX  
 PS Claim 2, Fig 291; 648pp; English.  
 XX  
 CC The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO134 and PRO186  
 CC stimulate adrenal cortical capillary endothelial growth. PRO136,  
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO132,  
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
 CC useful for treating cancerous tumours. PRO812 inhibits vascular  
 CC endothelial growth factor (VEGF) stimulated endothelial cell growth in  
 CC cells and is thus useful for inhibiting endothelial cell growth in  
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
 CC immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of  
 CC retinal neurons cells (PRO132 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpiformis or Crohn's  
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or redifferentiation of chondrocytes in culture and  
 CC are thus useful for treating sports injuries, and arthritis. This  
 CC sequence represents a novel human PRO protein polynucleotide.  
 XX  
 SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;  
 XX  
 QY Query Match 24.1%; Score 78; DB 25; Length 570;  
 Db Best local similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 246 GCGAGGACCGCGGTATAGAGGCTTGCGCTTGGCGGCGAGCCGAGTTCCCGCGGC 305  
 Db 1 GCGAGGACCGCGGTATAGAGGCTTGCGCTTGGCGGCGAGCGAGTTCCCGCGGC 60  
 QY 306 GCGCGAGCGCGCGCGCGCC 323  
 Db 61 GCGCGGAGCGCGCGCGCGCC 78  
 XX  
 ID RESULT 11  
 ABX80890  
 ID ABX80890 standard; cDNA; 570 BP.  
 AC  
 AC ABX80890;  
 XX  
 XX 22-Apr-2003 (first entry)  
 DT  
 XX Human secreted/transmembrane protein cDNA, #163.  
 DE  
 XX Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
 XX

KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;  
KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
XX Homo sapiens.  
XX US2003027162-A1.  
XX 06-FEB-2003.  
XX  
XX  
XX 15-NOV-2001; 2001US-0997428.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19337.  
PR 07-OCT-1998; 98WO-US21141.  
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PR 01-DEC-1999; 99WO-US28301.  
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PR 20-DEC-1999; 99WO-US30911.  
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PR 10-JUN-1998; 98US-088734P.  
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PR 10-JUN-1998; 98US-088742P.  
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PR 11-JUN-1998; 98US-088861P.  
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PR 12-JUN-1998; 98US-089105P.  
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QY 306 GCCCGGAGCCCGCGCGCC 323  
 Db 61 GCCCGGAGCCCGCGCGCC 78

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XX AC ABX90363;

DT 01-MAY-2003 (first entry)

XX Human secreted/transmembrane protein cDNA, #163.

KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;

XX Pharmaceutical; diagnostic; therapeutic; gene therapy.

OS Homo sapiens.

XX US2002160384-A1.

XX

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PD 31-OCT-2002.
XX 14-NOV-2001; 2001US-0992598.
XX 05-NOV-1997; 97WO-US20069.
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PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US05028.
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PR 02-JUN-1999; 99WO-US21090.
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PR 20-DEC-1999; 99WO-US30095.
PR 05-JAN-2000; 2000WO-US00213.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03365.
PR 18-FEB-2000; 2000WO-US04341.
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PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
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PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
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PR 09-JUN-1998; 98US-088655P.
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PR 18-JUN-1998; 98US-089908P.
PR 28-AUG-2001; 2001US-0941992.

XX (GERTH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers L, Eaton DL,
XX Ferrera N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
XX Girmaidi JC, Gurney AL, Kijavyn IJ, Napier MA, Pan J, Paoni NF,
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
XX Zhang Z;
XX WPI; 2003-288106/28.
XX P-PSDB; ABU60604.
XX
XX New transmembrane polypeptides and nucleic acids encoding the
XX polypeptides, useful in gene therapy, in chromosome identification, as
XX chromosome markers, or in generating probes -
XX
XX Claim 2; Fig 289; 650pp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
XX comprising a sequence without signal peptide and the nucleic acid
XX encoding them. The polypeptides can be used to raise antibodies that
XX specifically bind to the PRO polypeptide, for linking a bioactive
XX molecule to a cell expressing a PRO protein and for modulating at least
XX one biological activity of a cell. The PRO polypeptides or
XX polynucleotides are also useful in gene therapy, in chromosome
XX identification, as chromosome markers, or in generating probes. The PRO
XX polypeptides are useful as molecular markers for protein
XX electrophoresis, and the isolated nucleic acids may be used for
XX recombinantly expressing those markers. The PRO polypeptides and nucleic
XX acids may also be used in tissue typing. Anti-PRO antibodies are useful
XX in diagnostic assays for PRO, and in affinity purification of PRO from
XX recombinant cell culture or natural sources. The sequences presented in
XX ABX90083-ABX90468 are the genes encoding, the primers amplifying and the
XX probes detecting the PRO polynucleotides of the invention.
XX Note: The sequence data for this patent is also available in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
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XX Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;
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XX Best Local Similarity 100.0%; Fred No. 1.5e-07;
XX Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GCCCGAGCCCCGCC 78

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ID ABX77974 standard; cDNA; 570 BP.

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AC ABX77974;

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DT 14-APR-2003 (first entry)

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XX Human; PRO; gene; ss; cytosolic; tumour; cancer; breast; lung; stomach;

XX liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADPRT;

XX antibody-dependent enzyme mediated prodng therapy.

XX

OS Homo sapiens.

XX

PN US2003027163-A1.

XX

PD 06-FEB-2003.

XX

PD 15-NOV-2001; 2001US-0997666.

XX

PF 05-NOV-1997; 97WO-US20069.

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 KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;  
 KW Pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;  
 KW colon cancer; lung cancer; breast cancer; cancer; gene therapy.  
 OS Homo sapiens.  
 PN US2002142961-A1.  
 XX 03-OCT-2002.  
 XX 19-NOV-2001; 2001US-0989721.  
 PF 05-NOV-1997; 97WO-US20069.  
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 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06884.  
 PR 15-MAR-2000; 2000WO-US07377.  
 PR 20-MAR-2000; 2000WO-US08439.  
 PR 30-MAR-2000; 2000WO-US13358.  
 PR 15-MAY-2000; 2000WO-US13705.  
 PR 17-MAY-2000; 2000WO-US14042.  
 PR 22-MAY-2000; 2000WO-US14941.  
 PR 30-MAY-2000; 2000WO-US15264.  
 PR 02-JUN-2000; 2000WO-US20710.  
 PR 28-JUL-2000; 2000WO-US22031.  
 PR 11-AUG-2000; 2000WO-US23522.  
 PR 23-AUG-2000; 2000WO-US23528.  
 PR 24-AUG-2000; 2000WO-US30952.  
 PR 08-NOV-2000; 2000WO-US32678.  
 PR 01-DEC-2000; 2000WO-US36520.  
 PR 28-FEB-2001; 2001WO-US17800.  
 PR 01-JUN-2001; 2001WO-US19692.  
 PR 20-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 16-JUN-1997; 97US-049787P.  
 PR 17-OCT-1997; 97US-062250P.  
 PR 12-NOV-1997; 97US-065186P.  
 PR 13-NOV-1997; 97US-065311P.  
 PR 24-NOV-1997; 97US-066770P.  
 PR 25-FEB-1998; 98US-075945P.  
 PR 20-MAR-1998; 98US-078910P.  
 PR 28-APR-1998; 98US-083322P.  
 PR 07-MAY-1998; 98US-084600P.



PR 28-MAY-1998; 98US-087106P.  
 PR 02-JUN-1998; 98US-087607P.  
 PR 02-JUN-1998; 98US-087609P.  
 PR 02-JUN-1998; 98US-087659P.  
 PR 03-JUN-1998; 98US-087827P.  
 PR 04-JUN-1998; 98US-088021P.  
 PR 04-JUN-1998; 98US-088025P.  
 PR 04-JUN-1998; 98US-088026P.  
 PR 04-JUN-1998; 98US-088028P.  
 PR 04-JUN-1998; 98US-088029P.  
 PR 04-JUN-1998; 98US-088030P.  
 PR 04-JUN-1998; 98US-088033P.  
 PR 04-JUN-1998; 98US-088126P.  
 PR 05-JUN-1998; 98US-088157P.  
 PR 05-JUN-1998; 98US-088202P.  
 PR 05-JUN-1998; 98US-088212P.  
 PR 05-JUN-1998; 98US-088217P.  
 PR 05-JUN-1998; 98US-088655P.  
 PR 05-JUN-1998; 98US-088734P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088742P.  
 PR 10-JUN-1998; 98US-088810P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088826P.  
 PR 11-JUN-1998; 98US-088858P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089440P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 17-JUN-1998; 98US-089532P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089598P.  
 PR 17-JUN-1998; 98US-089599P.  
 PR 17-JUN-1998; 98US-089600P.  
 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.  
 (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 PI Ferrara N, Fong S, Gerber H, Gertlisen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurley AL, Kijavini IU, Napier MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;  
 XX WPI; 2003-155950/15.  
 DR P-PSDB; ABUS9026.  
 XX New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
 PT PRO361 or PRO846) useful as targets for therapeutic intervention in  
 PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers  
 PT -  
 XX Claim 2; Fig 289; 647pp; English.  
 PS  
 CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful as pharmaceuticals/diagnostics.  
 CC biosensors or bioreactors, for detecting or treating e.g. tumours in  
 CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or  
 CC rabbits as targets for therapeutic intervention in certain cancers (e.g.  
 CC colon, lung or breast cancers) and diagnostic determination of the  
 CC presence of these cancers. The PRO polypeptides are also useful as  
 CC molecular weight markers or for chromosome identification. The PRO genes

CC are useful as hybridisation probes or for screening libraries of human  
 CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
 CC therapy, particularly for replacing a defective gene. The sequences  
 CC presented in ABX79290-ABX79675 are the genes encoding, the primers  
 CC amplifying and the probes detecting the PRO polynucleotides of the  
 CC invention.  
 CC Note: The sequence data for this patent is also available in electronic  
 CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
 CC  
 XX Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;  
 XX  
 QY Query Match 24.1%; Score 78; DB 25; Length 570;  
 Db Best local similarity 100.0%; Pred. No. 1.5e-07; Mismatches 0; Gaps 0;  
 Matches 78; Conservative 0; Indels 0; Gaps 0;  
 QY 246 GCGAGACCGGCTTTAGAGAGCTTCTGCGCTTCCCGGACCGGAGTTCCCGGCC 305  
 Db 1 GCGAGACCGGCTTTAGAGAGCTTCTGCGCTTCCCGGACCGGAGTTCCCGGCC 60  
 QY 306 GCGCCGAGCCCGCGGCC 323  
 Db 61 GCGCCGAGCCCGCGGCC 78  
 RESULT 16  
 ABX64209  
 ID ABX64209 standard; cDNA; 570 BP.  
 AC  
 XX ABX64209;  
 XX  
 DT 26-FEB-2003 (first entry)  
 XX  
 DE cDNA encoding human PRO1245 polypeptide.  
 XX  
 KW Human; PRO polypeptide; secreted protein; transmembrane protein;  
 KW genetic disorder; antibacterial; immunosuppressive; transgenic;  
 KW gene therapy; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002103125-A1.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 20-NOV-2001; 2001US-0989731.  
 XX  
 PF 05-NOV-1997; 97WO-US20069.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 30-NOV-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 16-DEC-1999; 99WO-US28634.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 06-JAN-2000; 2000WO-US00219.  
 PR 11-FEB-2000; 2000WO-US03736.  
 PR 18-FEB-2000; 2000WO-US03565.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 02-MAR-2000; 2000WO-US05004.  
 PR 10-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07317.  
 PR 30-MAR-2000; 2000WO-US08439.

PR 15-MAY-2000; 2000MO-US13358.  
 PR 17-MAY-2000; 2000MO-US13705.  
 PR 22-MAY-2000; 2000MO-US14042.  
 PR 30-MAY-2000; 2000MO-US14941.  
 PR 02-JUN-2000; 2000MO-US15264.  
 PR 28-JUL-2000; 2000MO-US20710.  
 PR 11-AUG-2000; 2000MO-US22031.  
 PR 23-AUG-2000; 2000MO-US23522.  
 PR 24-AUG-2000; 2000MO-US23328.  
 PR 08-NOV-2000; 2000MO-US30952.  
 PR 01-DEC-2000; 2000MO-US32678.  
 PR 28-FEB-2001; 2001MO-US06520.  
 PR 01-JUN-2001; 2001MO-US17800.  
 PR 20-JUN-2001; 2001MO-US19692.  
 PR 29-JUN-2001; 2001MO-US21066.  
 PR 09-JUL-2001; 2001MO-US21735.  
 PR 16-JUN-1997; 97US-049787P.  
 PR 17-OCT-1997; 97US-062250P.  
 PR 12-NOV-1997; 97US-065186P.  
 PR 13-NOV-1997; 97US-065311P.  
 PR 24-NOV-1997; 97US-066770P.  
 PR 25-FEB-1998; 98US-075945P.  
 PR 20-MAR-1998; 98US-078910P.  
 PR 28-APR-1998; 98US-083322P.  
 PR 07-MAY-1998; 98US-084600P.  
 PR 28-MAY-1998; 98US-087106P.  
 PR 02-JUN-1998; 98US-087607P.  
 PR 02-JUN-1998; 98US-087609P.  
 PR 03-JUN-1998; 98US-087759P.  
 PR 04-JUN-1998; 98US-087827P.  
 PR 04-JUN-1998; 98US-088021P.  
 PR 04-JUN-1998; 98US-088025P.  
 PR 04-JUN-1998; 98US-088026P.  
 PR 04-JUN-1998; 98US-088028P.  
 PR 04-JUN-1998; 98US-088029P.  
 PR 04-JUN-1998; 98US-088030P.  
 PR 04-JUN-1998; 98US-088033P.  
 PR 04-JUN-1998; 98US-088336P.  
 PR 05-JUN-1998; 98US-088167P.  
 PR 05-JUN-1998; 98US-088202P.  
 PR 05-JUN-1998; 98US-088212P.  
 PR 05-JUN-1998; 98US-088217P.  
 PR 09-JUN-1998; 98US-088655P.  
 PR 10-JUN-1998; 98US-088734P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088742P.  
 PR 10-JUN-1998; 98US-088810P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088826P.  
 PR 11-JUN-1998; 98US-088858P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088876P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089440P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 17-JUN-1998; 98US-089532P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089598P.  
 PR 17-JUN-1998; 98US-089599P.  
 PR 17-JUN-1998; 98US-089600P.  
 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.  
 XX  
 XX  
 PR (GETH) GENENTECH LTD.  
 PI Ashkenazi AJ, Baker KP, Bolstein D, Deanyers L, Eaton DL,  
 PI Ferreira N, Fong S, Geisler H, Geisleren ME, Goddard A,  
 PI Grimaldi JC, Gurney AL, Kijavini IU, Napier MA, Fan J, Goddard PJ,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams FW, Wood WI;

PI Zhang Z;  
 XX WPI; 2003-102117/09.  
 DR P-PSDB; ABU13986.  
 XX  
 XX Novel secreted and transmembrane polypeptide for modulating biological  
 PT activity of cell expressing the polypeptide, identifying agonists or  
 PT antagonists of polypeptide, and as molecular weight markers  
 XX  
 PS Claim 2; Fig 289; 649pp; English.  
 XX The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The  
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides for  
 CC linking bioactive molecules to cells expressing PRO polypeptides,  
 CC for modulating biological activities of cells expressing PRO  
 CC polypeptides, and for identifying agonists or antagonists.  
 CC The polynucleotide sequences encoding PRO polypeptides are useful as  
 CC hybridisation probes, in chromosome and gene mapping, in the generation  
 CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for  
 CC generating transgenic animals or knockout animals, to construct  
 CC polypeptide, and for the genetic analysis of individuals with genetic  
 CC disorders, in gene therapy, for chromosome identification, as  
 CC chromosome markers, and for generating probes for PCR, Northern  
 CC analysis, Southern analysis and Western analysis. The present  
 CC sequence encodes a human PRO polypeptide of the invention.  
 CC Note: The sequence data for this patent was obtained in electronic  
 CC format directly from the USPRO web site at  
 CC seqdata.uspro.gov/psidentry.html.  
 XX  
 SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;  
 Query Match 24.1%; Score 78; DB 25; Length 570;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 246 GCGAGGACGGGATTAAGAGCCTGCTGCTGCGCGGAGCGGAGTTCCCGGCC 305  
 DB 1 CCGAGGACCGGATTAAGAGCCTGCTGCTGCGCGGAGCGGAGTTCCCGGCC 60  
 QY 306 GCGCGGAGCGCGCGGCC 323  
 DB 61 GCGCGGAGCGCGCGGCC 78  
 RESULT 17  
 ABX17173  
 ID ABX17173 standard; cDNA; 570 BP.  
 XX  
 AC ABX17173;  
 XX  
 DT 04-FEB-2003 (first entry)  
 XX  
 DE Human PRO polynucleotide #127.  
 XX  
 KW Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;  
 KW toxin; radiolabel; cell death; gene mapping; chromosome mapping;  
 KW protein electrophoresis; genetic disorder; immunosuppressive; cytostatic;  
 KW antibacterial.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002123463-A1.  
 PD  
 XX 05-SEP-2002.  
 BP 19-NOV-2001; 2001US-0989732.  
 XX  
 XX 05-NOV-1997; 97MO-US20069.  
 XX 16-SEP-1998; 98MO-US19350.  
 XX 17-SEP-1998; 98MO-US19437.

PR	07-OCT-1998	98MO-US211.048
PR	01-DEC-1998	98MO-US225.108
PR	05-JAN-1999	99MO-US501.060
PR	08-MAR-1999	99MO-US505.028
PR	02-JUN-1999	99MO-US122.952
PR	15-SEP-1999	99MO-US212.950
PR	10-NOV-1999	99MO-US215.447
PR	30-NOV-1999	99MO-US281.137
PR	01-DEC-1999	99MO-US283.814
PR	08-DEC-1999	99MO-US286.304
PR	16-DEC-1999	99MO-US300.095
PR	20-DEC-1999	99MO-US309.117
PR	06-JAN-2000	2000MO-US500.719
PR	05-JAN-2000	2000MO-US503.365
PR	11-FEB-2000	2000MO-US504.411
PR	18-FEB-2000	2000MO-US504.944
PR	22-FEB-2000	2000MO-US504.914
PR	24-FEB-2000	2000MO-US505.004
PR	10-MAR-2000	2000MO-US505.619
PR	10-MAR-2000	2000MO-US505.641
PR	15-MAR-2000	2000MO-US507.677
PR	20-MAR-2000	2000MO-US507.684
PR	30-MAR-2000	2000MO-US508.339
PR	15-MAY-2000	2000MO-US137.055
PR	17-MAY-2000	2000MO-US140.425
PR	30-MAY-2000	2000MO-US149.441
PR	02-JUN-2000	2000MO-US155.644
PR	28-JUN-2000	2000MO-US207.011
PR	11-AUG-2000	2000MO-US220.203.1
PR	23-AUG-2000	2000MO-US233.252
PR	24-AUG-2000	2000MO-US233.258
PR	08-NOV-2000	2000MO-US302.978
PR	01-DEC-2000	2000MO-US305.752
PR	28-FEB-2001	2001MO-US178.800
PR	01-JUN-2001	2001MO-US196.982
PR	20-JUN-2001	2001MO-US210.662
PR	09-JUL-2001	2001MO-US211.335
PR	16-OCT-1997	97US-049.676
PR	17-OCT-1997	97US-062.220
PR	12-NOV-1997	97US-065.186
PR	13-NOV-1997	97US-065.311
PR	24-NOV-1997	97US-066.774
PR	25-FEB-1998	98US-075.945
PR	20-MAR-1998	98US-078.910
PR	28-APR-1998	98US-083.322
PR	07-MAY-1998	98US-084.600
PR	28-MAY-1998	98US-087.106
PR	02-JUN-1998	98US-087.607
PR	02-JUN-1998	98US-087.609
PR	02-JUN-1998	98US-087.759
PR	03-JUN-1998	98US-087.872
PR	04-JUN-1998	98US-088.021
PR	04-JUN-1998	98US-088.025
PR	04-JUN-1998	98US-088.036
PR	04-JUN-1998	98US-088.037
PR	04-JUN-1998	98US-088.172
PR	05-JUN-1998	98US-088.202
PR	05-JUN-1998	98US-088.219
PR	05-JUN-1998	98US-088.257
PR	03-JUN-1998	98US-088.511
PR	10-JUN-1998	98US-088.734
PR	10-JUN-1998	98US-088.739
PR	10-JUN-1998	98US-088.742
PR	10-JUN-1998	98US-088.810
PR	10-JUN-1998	98US-088.843
PR	10-JUN-1998	98US-088.856

PR 11-JUN-1998 98US-0086816P  
PR 11-JUN-1998 98US-0086836P  
PR 11-JUN-1998 98US-0086861P  
PR 11-JUN-1998 98US-0086876P  
PR 12-JUN-1998 98US-0089105P  
PR 12-JUN-1998 98US-0089116P  
PR 16-JUN-1998 98US-0089404P  
PR 16-JUN-1998 98US-0089512P  
PR 16-JUN-1998 98US-0089521P  
PR 17-JUN-1998 98US-0089532P  
PR 17-JUN-1998 98US-0089538P  
PR 17-JUN-1998 98US-0089558P  
PR 17-JUN-1998 98US-0089599P  
PR 17-JUN-1998 98US-0089600P  
PR 17-JUN-1998 98US-0089631P  
PR 18-JUN-1998 98US-0089801P  
PR 18-JUN-1998 98US-0089907P  
PR 18-JUN-1998 98US-0089960P  
PR 28-AUG-2001 2001US-0094196Z

(GETH ) GENENTECH INC.

PI Abhkenazi AJ, Baker KP, Botstein D, Desroyers L, Eaton DL,  
PI Ferreira N, Fong S, Geberh H, Gerlitsen ME, Goddard A,  
PI Roymltd JC, Gurey AL, Kljavin ID, Napier MA, Pan J, Paout NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,  
PI Zhang Z,  
XX  
WPI; 2003-066810/06.  
DR  
P-PSDB; ABU10941.

PT Novel screened and transmembrane polypeptide for modulating biological  
PT activity of cell expressing the polypeptide, identifying agonists or  
PT antagonists of polypeptide, and as molecular weight markers -  
XX  
Claim 2, Fig 289, 655pp; English.

The invention relates to a secreted and transmembrane polypeptide, termed PRO polypeptide, and the polynucleotide encoding it. The polypeptide is useful for detecting PRO polypeptides and for linking a bioactive molecule to a cell expressing the above polypeptides, where the bioactive molecule is a toxin, radiolabel or an antibody. The bioactive material causes the death of the cell. The polypeptide is useful for identifying agents or antagonists of the PRO polypeptide, for preparing variants of PRO, as a molecular weight marker for protein electrophoresis purposes and the PRO polynucleotide is useful for recombinantly expressing those markers. The polynucleotide is also useful as a hybridisation probe, in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, to construct hybridisation probes for mapping the gene which encodes PRO, and for the genetic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, as a chromosome marker and for generating probes for PCR, Northern analysis, Southern analysis and Western analysis. This sequence represents a human PRO polynucleotide of the invention.

**SQ** Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;

Query Match	Score	DB	Length
24.1%	78	25	570

```

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

Dy 246 GCGAGGACCGGGGTATTAAGAACCCTGTGGCCTTGCCCGGCAGGCCGAGTTCCCCCGC 305

Dd 1 GCGAGGACCGGGGTATTAAGAACCCTGTGGCCTTGCCCGGCAGGCCGAGTTCCCCCGC 60

QY	306	GCCCCGAGCCCCCGGCC	323
Db	61	GCCCCGAGCCCCCGGCC	78

RESULT 18  
AAV54617









XX 07-MAR-2002.  
 PD 01-SEP-2001; 2001WO-EPI0074.  
 PF 01-SEP-2000; 2000DE-1043826.  
 PR 05-SEP-2000; 2000DE-1044543.  
 XX (EPIC-) EPICENOMICS AG.  
 PA  
 PI Olek A, Piepenbrock C, Berlin K, Guettig D,  
 DR WPI; 2002-371829/40.

PT Determining the degree of cytosine methylation in genomic DNA, useful  
 for diagnosis and prognosis, comprises selective hybridization of  
 PT amplicons from chemically treated DNA -

PS Claim 12; 56pp + Sequence Listing; 56pp; German.

CC This invention describes a novel method for determining the degree of  
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
 CC genomic sample of DNA. The sample is treated chemically to convert  
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
 CC DNA that contains the target C is amplified to form a labeled amplicon.  
 CC The amplicon is hybridized to two classes, each with at least one  
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers  
 CC and the degree of hybridization to both classes is determined from the  
 CC label on the amplicon. From the ratio of labels hybridized to the two  
 CC classes of oligomers, the degree of methylation is calculated. The method  
 CC is used: (i) for diagnosis and/or prognosis of side effects of  
 CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders  
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory  
 CC systems etc.; particularly by detecting mutations or single nucleotide  
 CC polymorphisms (SNPs) and (ii) for differentiation of cell or tissue  
 CC types and for investigating cell differentiation. The method allows the  
 CC methylation status of many C residues to be determined simultaneously.  
 CC AB013410-AB054121 represent genomic DNA sequences used to illustrate the  
 CC method for determining the degree of cytosine methylation described in  
 CC the disclosure of the invention.

XX Sequence 629 BP; 164 A; 319 C; 100 G; 46 T; 0 other;

Query Match 16.2%; Score 52.2; DB 24; Length 629;  
 Best Local Similarity 50.2%; Pred. No. 0.033;  
 Matches 129; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 1 GCGCGTGGGTCAACCCGCAAGCGAAGTCCGGGCGGGTGGGCTTCGCGGAGCAAA 60  
 DB 347 GCGGTGG 288  
 QY 61 GCGCGGCTCTCTCTCTCAAGAGGGCCCGCAGCGCTTCCAGAGGAAGTCTTCAGAGCC 120  
 DB 287 GGG 228  
 QY 121 GGGGAGGAGGAGGGGGGCGAGCGGCTTCCAGAGGGCCCGCGCGAGCAGGAAGTTGGCCAG 180  
 DB 227 GGG 168  
 QY 181 GGCACGGCCGTGACCGGAGCGGCGGAGGGCTTTCACAGAGCCGGGGCGAGAGCCGGGGCTG 240  
 DB 167 GGGCGGG 108  
 QY 241 GAGGGGGCGAGAGCCGGG 257  
 DB 107 CGGGGGCGGGGGCGGGG 91

RESULT 25  
 AAX53491/c  
 ID AAX53491 standard; DNA; 114955 BP.  
 XX AC AAX53491;

XX 05-JUL-1999 (first entry)  
 DT Human adenosine A1 receptor antisense oligonucleotide fragment.  
 DE Antisense oligonucleotide; multiple target; antisense treatment;  
 XX impaired respiration; inflammation; lung disease;  
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
 KW acute asthma; allergy; asthma; impeded respiration;  
 KW respiratory distress syndrome; pain; cystic fibrosis;  
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
 KW prostate cancer; ss.

OS Synthetic.

XX WO911886-A1.

XX 25-MAR-1999.

XX 17-SEP-1998; 98WO-US19419.

XX 09-JUN-1998; 98US-0093972.

XX 17-SEP-1997; 97US-0059160.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nye JW;

XX WPI; 1999-229400/19.

XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
 XX vasoconstriction

XX Disclosure; Page 37; 120pp; English.

CC The specification describes antisense oligonucleotides (AAX52869-X55271)  
 CC directed against at least 2 mRNAs selected from target genes, coding and  
 CC non-coding regions of RNAs corresponding to target genes, gene  
 CC initiating regions, genomic flanking regions, intron-exon borders, the  
 CC 5' end, the 3' end and the juxta-section between coding and non-coding  
 CC regions and all segments of RNAs encoding proteins associated with one  
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides  
 CC may be derived from sequences AAX5272-74. These multiple target  
 CC oligonucleotides (specifically AAX5180-271) can be used for the  
 CC antisense treatment of diseases and conditions. Typical diseases and  
 CC conditions are those associated with impaired respiration and  
 CC inflammation, including lung diseases, pulmonary vasoconstriction,  
 CC inflammation, allergic rhinitis, acute asthma, pain, cystic fibrosis,  
 CC respiration, respiratory distress syndrome, emphysema, chronic  
 CC obstructive pulmonary disease (COPD), and cancers such as leukemias,  
 CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,  
 CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,  
 CC or have metastasized to the lungs, including breast and prostate cancer.

XX Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;

Query Match 14.8%; Score 47.8; DB 20; Length 114955;  
 Best Local Similarity 45.3%; Pred. No. 0.24;  
 Matches 126; Conservative 9; Mismatches 140; Indels 3; Gaps 1;

QY 8 GGGTCAACCCGCAAGCGAAGTCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 67  
 DB 107160 GGGCGGGGGGGGCAAGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 107104  
 QY 68 CCGTCTCTCTCAAGAGGGCCCGCAGCGCTTCCAGAGGAAGTCTTCAGAGCCCGGGCAGG 127  
 DB 107103 CAAGCGGG 107044



QY 128 GAAGGGGACAGGCTTCCAGAGGCGCGCCGACAGAGAAATTGGCCAGGGCAGCG 187  
 DB 107043 GGGCCGACCCAGNNNNNNNNCCGGGCGCGGCAAGCCGGCCGGGGCCGAGCCAGG 106984  
 QY 188 CCGTAGCGGAGCGGCGGCTTTCTCAGAGCGCGCGGCGCGCTGAGAGGCGC 247  
 DB 106983 NNHHNNNSCCGGGCGCGGCGGCGAGCCGGGCGCGGCGGCGGCGGCGG 106924  
 QY 248 GAGGACCGGCTATAGAGAGCTCGTGGCTTGGCCCGGG 285  
 DB 106923 GCGGGCGCGGCAAGCCGGGCGCGGCGCGGCGGCGGCGGCGGCGGCGG 106886

RESULT 26  
 ID ABN81321 standard; cDNA, 3743 BP.  
 AC ABN81321;  
 XX 30-AUG-2002 (first entry)  
 DE Human mast cell related gene F10317 SEQ ID NO 6.  
 XX  
 KW Human; mast cell; MC; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW vasoactive; dermatological; allergy; hypersensitivity; rhinitis; asthma;  
 KW gene; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 377..1951  
 FT /tag= a  
 FT /product= "MC17"  
 XX  
 PN MO200246389-A2.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PP 07-DEC-2001; 2001WO-USA6180.  
 XX  
 PR 08-DEC-2000; 2000US-251835P.  
 PR 14-MAR-2001; 2001US-275479P.  
 PR 28-MAR-2001; 2001US-279115P.  
 PR 02-APR-2001; 2001US-280143P.  
 XX  
 PA (UNIO) UCB SA.  
 XX  
 PI Nocka K, Pirozzi G, Einstein R;  
 XX  
 DR WPI; 2002-508560/54.  
 DR P-PSDB; ABB77572.  
 XX  
 PT Novel isolated nucleic acids that are differentially expressed in mast  
 PT cells in patients with allergic hypersensitivity, encoding proteins  
 PT associated with mast cell degranulation and allergic hypersensitivity  
 PT  
 XX  
 PS Claim 1; Page 104-108; 119pp; English.  
 XX  
 CC The invention relates to isolated nucleic acid (ABN81319-ABN81324)  
 CC corresponding to genes differentially expressed in mast cells following  
 CC activation or in patients with allergic hypersensitivity disease, (I) a  
 CC that encodes proteins (ABN7569-ABN7575) (II) or a protein fragment of  
 CC (II) if at least amino acids (II) is useful for identifying binding  
 CC partners. (I) or (II) is useful for diagnosing or treating a disease  
 CC state (e.g. allergic hypersensitivity, seasonal rhinitis, asthma,  
 CC urticaria or atopic dermatitis or mastocytosis) in a subject which  
 CC involves determining the level of expression of (I) or (II). A computer  
 CC system, comprising a database containing information identifying the  
 CC expression level in a tissue or at least one mast cell of (I), is useful  
 CC for presenting information to identify the relative expression level of  
 CC (I). (II) is used as a marker to detect, diagnose or identify an allergic  
 CC response in a patient. The protein can also serve as a target that

CC modulate gene expression or activity and as an antigen to raise  
 CC polyclonal or monoclonal antibodies. (II) is useful for identifying  
 CC agents that modulate expression of the protein or agents, such as  
 CC agonists or antagonists. The agonists or antagonists are useful for  
 CC modulating biological activity and function of (II) and thus are useful  
 CC for alleviating disease conditions such as allergic hypersensitivity,  
 CC seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis.  
 XX

Sequence 3743 BP; 778 A; 1088 C; 1134 G; 743 T; 0 other;  
 Query Match 14.7%; Score 47.6; DB 24; Length 3743;  
 Best Local Similarity 46.9%; Pred. No. 0.28; Mismatches 169; Indels 0; Gaps 0;  
 Matches 149; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 3 GCGTGGGCTCAGACCGGCAAGAGAGTGGCGGGTGGCGGCGGAGAGCAAG 62  
 DB 381 GCCATGCCCCGACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 322  
 QY 63 CCGGCTCTGCTTCTCAAGAGGCGCCGAGCGCTGCGCAAGAGAGTCTCAAGCGCGG 122  
 DB 321 CCGGCTCTGAGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 262  
 QY 123 GCAGGAGAGGAGGCGGAGGCTTCCAGAGGCGCGCGCGCGCGCGAGAGAGTTGGCCAGG 182  
 DB 261 GCG 202  
 QY 183 CACGCGCTGAGCGGAGCGGCGGCGGCTTCTCAGAGGCGCGGCGCGCGCGCGCGCGCG 242  
 DB 201 GAAGCCGCTCGAGGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 142  
 QY 243 GGGGCGAGAGCGGCTATAGAGAGCTCTGCGCTTGGCGCGGCGAGCGCGAGTTCCCGG 302  
 DB 141 GCGGGGCTGGCAGAGGCGGAGCCGAGAGCGGCGGAGAGAGGCTGCGCGCGCGCGCG 82  
 QY 303 CCGGCGCGGAGCG 320  
 DB 81 CCG 64

RESULT 27  
 AAF44725  
 ID AAF44725 standard; cDNA, 2461 BP.  
 AC AAF44725;  
 XX  
 DT 27-MAR-2001 (first entry)  
 XX  
 DE Novel protein kinase cDNA, SEQ ID NO: 106.  
 XX  
 KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;  
 KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;  
 KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;  
 KW immune disorder; cardiovascular disease; neurodegenerative disease;  
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;  
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200073469-A2.  
 XX  
 PD 07-DEC-2000.  
 XX  
 PR 26-MAY-2000; 2000MO-US14842.  
 PR 28-MAY-1999; 99US-0136503.  
 XX  
 PA (SUGR-) SUGEN INC.  
 XX  
 PI Plowman GD, Martinez R, Whyte D, Sudersanam S;  
 XX  
 DR WPI; 2001-032161/04.  
 DR P-PSDB; AAB56597.  
 XX

PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and  
PT treating immune-related diseases and disorders, cardiovascular disease,  
PT neurodegenerative diseases and/or cancers -  
XX  
XX  
PS Example 1; Fig 2; 310p; English.  
XX  
XX The present sequence encodes a novel protein kinase. The nucleic acids  
CC and the protein kinases they encode may be used in the treatment and  
CC diagnosis of diseases associated with inappropriate kinase expression  
CC such as immune-related diseases and disorders, cardiovascular disease,  
CC neurodegenerative diseases and/or cancers. The nucleic acids and  
CC complementary sequences may also be used as DNA probes in diagnostic  
CC assays. The kinase polypeptides may be used as antigens in the production  
CC of antibodies of kinase expression and activity. Anti-kinase antibodies  
CC and kinase antagonists may also be used to down regulate kinase  
CC expression and activity. Diseases related to kinase expression and  
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune  
CC disorders, complications of organ transplantation, myocardial infarction,  
CC immune disorders, cardiomyopathies, strokes, renal failure,  
CC oxidative-stress related disorders, chronic inflammatory bowel disease,  
CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,  
CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and  
CC reproductive disorders.  
XX  
SQ Sequence 2461 BP; 426 A; 771 C; 811 G; 453 T; 0 other;  
Query Match 14.6%; Score 47; DB 22; Length 2461;  
Best Local Similarity 47.7%; Pred. No. 0.38;  
Matches 137; Conservative 0; Mismatches 150; Indels 0; Gaps 0;  
OY 37 CGGGTGGGCTTCGCGAGACAAGGCGGGCTGCTCTCTCAAGAGGCCCGCCAGCGCT 96  
DB 224 CGGGTGGGAGCTTCGAGAGCGGCGGCACTCCCTTGAAGCTTCGCGGGCCCGGGTGGCG 283  
OY 97 GCCAAGAGAGTCTTCGAGGCGCGGCGAGGAGGAGGCGGCTTCCAGAGCGCGC 156  
DB 284 GCGGTGCGGGGCGCGGGGAGCTGGCCCGGCAATTCGGGCGGCTTCGAGAGGTGC 343  
OY 157 CGGCGCGAGAGAGTTCGCGAGGCGCGGCGGCGGCGGCGGCGGCTTCTTCA 216  
DB 344 AGCGGTATTCGCGGGGCGCGCGCGCGCGCGCGCGCGGCGGCGGCGCGCGCTGA 403  
OY 217 GAGGCGGCGGCGCGCGCGCGCTGAGAGGCGGCGAGACCGGCTTCTTGGCC 276  
DB 404 TGGACTGCTCTCGGGGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCC 463  
OY 277 TTGCGCGGCGAGCGGAGTTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 323  
DB 464 TGTCCGAGCGGCGCGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 510  
RESULT 28  
ABI9477  
ID ABI9477 standard; cDNA; 1729 BP.  
XX  
XX ABI9477;  
AC  
XX  
XX 07-MAR-2002 (first entry)  
DT  
XX  
XX Mouse ischaemic condition related cDNA sequence SEQ ID NO:435.  
DE  
XX  
XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
KW vasoospastic ischaemia; ischaemic condition; ischaemic disease; ss.  
XX  
XX Mus musculus.  
OS  
XX  
XX WO20018188-A2.  
PN  
XX  
XX 22-NOV-2001.  
PD  
XX  
XX 18-MAY-2001; 2001WO-JP04192.  
PF  
XX  
XX 18-MAY-2000; 2000JP-0145977.  
PR

XX  
XX (UNYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
PA  
XX  
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
PI  
XX  
XX WPI; 2002-034733/04.  
DR  
XX  
XX P-PSDB; ABB57179.  
PT  
XX  
XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
PT expression levels of particular genes defined in the specification or  
PT by determining the expression profile of a gene group comprising these  
PT genes -  
XX  
XX Claim 2; Page 1194-1197; 2690p; English.  
PS  
XX  
XX The present invention describes a method for examining ischaemic  
CC conditions, comprising measuring the expression levels of particular  
CC genes (I) in a test sample or determining the expression profile of a  
CC gene group in the sample comprising genes selected from (I). The method  
CC is useful for examining the ischaemic condition (e.g. compressive  
CC ischaemia, occlusive ischaemia or vasoospastic ischaemia) by measuring  
CC expression levels of particular genes (ABI99202 to ABI99912, encoding  
CC the protein sequences in ABB57020 to ABB57374) or by determining the  
CC expression profile of a gene group comprising these genes. The  
CC expression levels or expression profiles produced by these genes are  
CC used as an indicator when screening for ischaemic condition-improving  
CC drugs or therapeutics for ischaemic diseases. ABI9913 and ABI9914  
CC represent PCR primers for a mouse ischaemic condition related sequence,  
CC which are used in the exemplification of the present invention.  
XX  
SQ Sequence 1729 BP; 367 A; 548 C; 529 G; 283 T; 2 other;  
Query Match 14.1%; Score 45.4; DB 24; Length 1729;  
Best Local Similarity 51.2%; Pred. No. 0.83;  
Matches 103; Conservative 1; Mismatches 97; Indels 0; Gaps 0;  
OY 122 GGCAGGGAAGGGGCAAGGCTTCCAGAGCGCGCGCGCGCGAGGAGTGGCCAGG 181  
DB 104 GGCAGGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 163  
OY 182 GCACGCGCTTGAAGCGAGCGGCGGCGGCTTCTCAAGAGCGGCGGAGCGCGCGCTGG 241  
DB 164 GCGGCGGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 223  
OY 242 AGGCGCGAGAGACCGGCTTGAAGAGCTCTGCGCTTCCCGGCGAGCGCGAGTTCGCC 301  
DB 224 GAGCGCGAGCGCGCGAGCGCGAGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCG 283  
OY 302 GCGGCGCGCGAGCG 322  
DB 284 CCGGCTTCGCGGCTCGCGCGCG 304  
RESULT 29  
AAT75036/c  
ID AAT75036 standard; cDNA; 3937 BP.  
XX  
XX AAT75036;  
AC  
XX  
XX 07-OCT-1997 (first entry)  
DT  
XX  
XX Chick fringe A (radical) protein cDNA.  
DE  
XX  
XX Fringe A; radical fringe; fate specification; neural tube;  
KW apical ectodermal ridge; cell proliferation; vasculature;  
KW atherosclerosis; tumour; wound healing; therapy; ss.  
XX  
XX Gallus sp.  
OS  
XX  
XX Key Location/Qualifiers  
FH misc\_difference 42..43  
FT /\*tag= a  
FT /note= "there may be an additional nucleotide



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Query Match 13.7%; Score 44.4; DB 24; Length 1503841;

Best Local Similarity 50.0%; Pred. No. 1.1; Matches 111; Conservative 0; Mismatches 0; Gaps 0;

```
QY      2      CGCGTGGGTCAGACCGCAAGAGTGCGGGCCGGGTGGGCTCCGCGAGACAAG 61
DB      244224 CTGGGGCGACAGAGAGAGAGAGCGCGCGGGGACCGCGGAGACCCACATC 244283
QY      62      GCGGGCGCTGCTCTCTCAAGAGGCCCGCAGCGCTGCGCAAGAGAGTCTCTGAGGCCG 121
DB      244284 GCGGGTCCCGCTCCGCTCCGCGACAGCAATGGGGAAGAAGCGCGGGCCGAGTTGGC 244343
QY      122     GGCAGGGAAGGGCGACGGCTTCCAGAGGCCCGCGCGCGCGAGCAAGAGTGGCCAGG 181
DB      244344 CACAGGTAAACAGGCTGGCAGAGCGCAGACGCTGCGCGCGCGCCACCCAGCGATT 244403
QY      182     GCACGCCCTGAGGGAGCGGCGAGGGCTTCTCAGAGGCC 223
DB      244404 TCAGGCAAGCACTCGCTCCAGGGCTCTCTCCGCGC 244445
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RESULT 31  
ABT01503  
ID ABT01503 standard; DNA; 1503841 BP.

```
XX AC ABT01503;
XX 07-NOV-2002 (first entry)
XX
XX DE Human neuregulin 1 gene.
XX
XX KM Human; neuregulin 1; neuregulin-1-associated gene 1; NRGL, NRGL1,
XX schizophrenia; chromosome 6p12; single nucleotide polymorphism; SNP;
XX neuroleptic; gene therapy; gene; db.
XX
XX OS Homo sapiens.
XX
XX FH Location/Qualifiers
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XX FT /product= "neuregulin 1"
XX FT /note= "this sequence contains introns"
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FT      exon        /number= 3
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FT      /*tag=| bi
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FT      634442..635331
FT      /*tag=| bj
FT      /number= 4a

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	Query Match	Similarity	Score	No. 4, 1, 2	DB 24,	length	1503841,
	Best Local	Similarity	50.0%	Pred.	1.1,		
	Matches	111;	Conservative	0;	Mismatches	111;	Indels
							Gaps
							0;
Qy	2	CGGCTGGGCTCAACCGCAAGCGTGGCGGGCGGGCTTCGCGGAGACAAAG	61				
Db	244224	CTCGGGCGGACAGAGAGAGAGCGCGCGGGAGACGGGAGCCCAAGAGACCCTC	2442833				
Qy	62	GCGGGCGTCCCTCTCTCAAGAGGCGCCGCGCTCCCAAGAGAACTCTTCAGAGCCG	121				
Db	244284	GCGGGTCCCGCTCGCTCCGCGACGACAGCTAGGGAGAAAGACGCGCGGCCAATTTGGAC	2443433				
Qy	122	GCGAGGAGAGGGGCGACAGGGCTTCCAGAGGCCCGCGCTCAGAGAAATTGGCCAGG	181				
Db	244344	CAACGGTAACAGAGCTGGCGCAGAGCGCAGGACCTGTCTCGCGCGGCGACCCACCGATT	2444030				
Qy	182	GCAAGCGCTGAGCGGAGCGGGCGAGGGCTTTCTCAGAGCGC	223				
Db	244404	TCCAGGACCAACTCCGCGCTCCAGAGGCTCTCTCTCCCTGCGC	244445				

ID	AAK95240	standard; DNA; 1503900 BP.
XX	AAK95240;	
XX	17-DEC-2001	(first entry)
XX	Human	neuregulin-1 gene.
XX	Human	neuregulin-1 associated gene 1; NRX1A1; Schizophrenia gene;
XX	gene therapy; ds.	
XX	Homo sapiens.	
XX	MO200164876-A2.	
XX	07-SEP-2001.	
XX	28-FEB-2001;	2001WO-US06376.
XX	28-FEB-2000;	2000US-0515715.
XX	(DECO-)	DECODE GENETICS EHF.
XX	Stefansson H,	Steinhorstodottir V, Gulcher JR,
XX	WPI; 2001-550179/61.	
XX	P-PSDI; AAG67900,	AAG67901, AAG67902, AAG67903, AAG67904, AAG67905,
XX	AAG67906, AAG67907,	AAG67908, AAG67909, AAG67910, AAG67911, AAG67912,
XX	AAG67913, AAG67914,	AAG67915, AAG67916, AAG67917, AAG67918, AAG67919,
XX	AAG67920, AAG67921,	AAG67922, AAG67923, AAG67924, AAG67925, AAG67926,
XX	AAG67927, AAG67928,	AAG67929, AAG67930, AAG67931, AAG67932, AAG67933,
XX	AAG67934, AAG67935,	AAG67936, AAG67937.
XX	Neuregulin-1-associated gene 1	nucleic acids and fragments, useful for
XX	preventing diagnosing and treating	schizophrenia -
XX	Disclosure; Page 90-501;	750pp; English.
XX	This sequence represents the human	neuregulin-1 associated gene 1
XX	(NRX1A1) of the invention. The NRX1A1	gene is also referred to as the
XX	human Schizophrenia gene. The invention	also relates to fragments or
XX	variants of the gene and the NRX1A1	polypeptides they encode. The
XX	NRX1A1 nucleic acids and polypeptides	may be used in the prevention,
XX	diagnosis and treatment of diseases	associated with inappropriate NRX1A1
XX	expression. For example, they may be	used to treat disorders associated
XX	with decreased expression by rectifying	mutations or deletions in a
XX	patient's genome that affect the activity	of NRX1A1 by expressing of
XX	inactive proteins or to supplement the	patients own production of
XX	NRX1A1. Additionally, the gene may be	used to produce NRX1A1
XX	polypeptides, by inserting the nucleic	acids into a host cell and
XX	culturing the cell to express the	protein. The gene may also be used as
XX	DNA probes and primers in diagnostic	assays to detect and quantitate the
XX	presence of similar nucleic acids in	samples, and therefore which
XX	patients may be in need of restorative	therapy. The NRX1A1 polypeptides
XX	may also be used as antigens in the	production of antibodies against
XX	NRX1A1 and in assays to identify	modulators of NRX1A1 expression and
XX	activity. Anti-NRX1A1 antibodies and	antagonists may also be used to
XX	down regulate expression and activity.	Anti-NRX1A1 antibodies may
XX	also be used as diagnostic agents for	detecting the presence of NRX1A1
XX	polypeptides in samples. NRX1A1 is	associated with schizophrenia which
XX	may be prevented, diagnosed and/or	created by the above methods.
XX	Sequence 1503900 BP; 452487 A;	281874 C; 288074 G; 480092 T; 1373 other;
XX	Query Match 13.7%; Score 44.4;	DB 22; Length 1503900;
XX	Best Local Similarity 50.0%;	Prod. No. 1.1.
XX	Matches 111; Conservative 0;	Mismatches 111; Indels 0; Gaps 0







XX 20-JUL-1999 .(first entry)  
XX  
DE Human 3-OST-4 encoding DNA.  
XX  
KW Heparan sulfate D-glucosaminyl 3-O-sulfotransferase; anticoagulant;  
KW saccharide; glycosaminoglycan; proteoglycan; antithrombotic; 3-OST;  
KW heparan sulfate; thrombotic disorders; deep vein thrombosis;  
KW pulmonary embolism; coagulation enzyme inactivation; ss.  
XX  
OS Homo sapiens.  
XX  
PM WO922005-A2.  
XX  
PD 06-MAY-1999.  
XX  
PF 23-OCT-1998; 98WO-US22597.  
XX  
PR 31-OCT-1997; 97US-0065437.  
XX  
PR 24-OCT-1997; 97US-0062762.  
XX  
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
XX  
PI Fritze IMS, Liu J, Rosenberg RD, Schwartz JJ, Shworak NW;  
PI Zhang L;  
XX  
DR WPI, 1999-312968/26.  
XX  
DR P-PsDB; AA117067.  
PT Heparan sulfate D-glucosaminyl 3-O-sulfotransferase and related  
PT polynucleotide  
PS Claim 5; Page 86-89; 95pp; English.

The invention relates to nucleic acid molecules (AMX37245-X37250) encoding heparan sulfate D-glucosaminyl 3-O-sulfotransferases (3-OSTs). The 3-OST proteins can be used for 3-O-sulfating saccharide residues within a preparation of glycosaminoglycan or proteoglycan polysaccharides. 3-OST-1 can be used for enriching the antithrombin-binding fraction in a preparation of heparan sulfates (HS). 3-OST-1 can also convert HS proteoglycan anticoagulant precursor to the HS anticoagulant (Hsact). The 3-OSTs (optionally lacking enzymatic function) can be used to determine partial sequence information for complex polysaccharides. The 3-OST proteins, genes and antibodies are also useful for diagnosis of disorders involving HS biosynthesis. 3-OSTs are especially used to generate anticoagulant pentasaccharides, which may be used to treat thrombotic disorders such as deep vein thrombosis and pulmonary embolism. Coagulation enzyme inactivation by antithrombins is enhanced by complexing of antithrombin with endothelial cell surface HS proteoglycans. This is responsible for the non-thrombogenic properties of blood vessels. The present sequence represents a human 3-OST-4 encoding DNA.

Sequence 3658 BP; 771 A; 1085 C; 1107 G; 695 T; 0 other;

Query Match 13.6%; Score 44; DB 20; Length 3658;  
Best Local Similarity 50.5%; Pred. No. 1.6;  
Matches 107; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

111 CTCGAGGCCCGGGCAGGGGAAGGGGCA CGGGCTTCCACAGGGCGCGGCAGCAGAGA 170  
Db CTTCGGCGGGAGCAGCGTCGTGGGGGGGGGCGCATCGCGCTCCCTTGCCCAACGGGA 679

171 AGTTGGCCAGGCGACAGCGCCGTATAGAGAGCGGCGCAGAGGCTTCTCAGAGCGCCGGCCAG 230  
Qy CAGCGCCAGAGGCCCCGGGGCGCGACGCGCTCTTCATTATGACACCGAGCGCGCTGGCACG 739

231 GCCGGCGCTGAGAGGGGCGCAGAGACC GGGTATTAAGAACTCTGTGGCTTCCCTGGGCGAGC 290  
Qy GCGGGCGGGGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGAACAACATGTCCGGGAGCG 799

231 GCAGGTTCCCG 322

DB	800	CCGGGAGCTGCCTCGCAGCGCGCGCGCGCGCGC 831
RESULT 37		
ID	AAK37251	
AC	AAK37251 standard; DNA; 4045 BP.	
XX	AAK37251;	
DT	20-JUL-1999	(first entry)
DE	Human 3'-OST-4 5' promoter and exon sequence.	
KM	Heparan sulfate D-glucosaminyl 3-O-sulfotransferase; anticoagulant;	
KW	saccharide; glycosaminoglycan; proteoglycan; antithrombin; 3-OST;	
KM	heparan sulfate; thrombotic disorder; deep vein thrombosis;	
KW	pulmonary embolism; coagulation enzyme inactivation; ss.	
OS	Homo sapiens.	
PX	WO922005-A2.	
PN	06-MAY-1999.	
PD	23-OCT-1998;	98WO-US22597.
PX	31-OCT-1997;	97US-0065437.
PR	24-OCT-1997;	97US-0062762.
PA	(MASI ) MASSACHUSETTS INST TECHNOLOGY.	
XX	Fitzte LMS, Liu J, Rosenberg RD, Schwartz JJ, Shworak NW;	
PI	Zhang L,	
DR	WPI, 1999-312966/26.	
XX	Heparan sulfate D-glucosaminyl 3-O-sulfotransferase and related	
PT	polynucleotides	
BS	Claim 60; Page 93-95; 95pp; English.	
XX	The invention relates to nucleic acid molecules (AAK37245-X37250)	
XX	encoding heparan sulfate D-glucosaminyl 3-O-sulfotransferases (3-OSTs).	
CC	The 3-OST proteins can be used for 3-O-sulfating saccharide residues	
CC	within a preparation of glycosaminoglycan or proteoglycan	
CC	polyasaccharides. 3-OST-1 can be used for enriching the	
CC	antithrombin-binding fraction in a preparation of heparan sulfates (HS).	
CC	3-OST-1 can also convert HS proteoglycan anticoagulant precursor to the	
CC	HS anticoagulant (HSAc). The 3-OSTs (optionally lacking enzymatic	
CC	function) can be used to determine partial sequence information for	
CC	complex polyasaccharides. The 3-OST proteins, genes and antibodies are	
CC	also useful for diagnosis of disorders involving HS biosynthesis. 3-OSTs	
CC	are especially used to generate anticoagulant pentasaccharides, which may	
CC	be used to treat thrombotic disorders such as deep vein thrombosis and	
CC	pulmonary embolism. Coagulation enzyme inactivation by antithrombin is	
CC	enhanced by complexing of antithrombin with endothelial cell surface HS	
CC	proteoglycans. This is responsible for the non-thrombogenic properties	
CC	of blood vessels. The present sequence represents a human 3-OST-4	
CC	5' promoter and exon sequence.	
SQ	Sequence 4045 BP; 823 A; 1150 C; 1277 G; 795 T; 0 other;	
Query Match	13.6%;	Score 44; DB 20; Length 4045;
Best Local Similarity	50.5%;	Pred. No. 1.6';
Matches 107;	Conservative 0;	Mismatches 105; Indels 0; Gaps 0;
OY	111 CTGAGGCCCGGGGCAAGAGGGGCGACGGGCTTCCAGAGGCCCGCGCGCGAGCAGA 170	
DB	2619 CTCGGCGGGCACGGTCGTGGGCGGGGGGCCATACGGGCGGGCTCCCCCTTGCGCGAGGGA 2678	
OY	171 AGTTGGCCAGGGCGACGGCCGTAGCGGAGCGCGGAGGACTTTCTCAGAGAGCGCGGCGAG 230	
DB	2679 CAGCGCGCGAGGGCGGGGGCGCGACGGCGGTGCTTCATGCAAGCCGGGCGCGGCTTAGCAGC 2738	



CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
 CC (AAK80020) are omitted as the relevant pages from the sequence listing  
 CC were missing at the time of publication.  
 XX  
 SQ Sequence 2834 BP; 540 A; 1007 C; 919 G; 368 T; 0 other;  
 Query Match 13.6%; Score 43.8; DB 22; Length 2834;  
 Best Local Similarity 51.0%; Pred. No. 1.7; Mismatches 122; Indels 5; Gaps 1;  
 Matches 132; Conservative 0; Mismatches 122; Indels 5; Gaps 1;  
 QY 55 GACAAAGGCGGCGCTGCTCTCTCAAGAGGCGCCAGCGCTTCCAGAGAAAGTCTTCG 114  
 DB 1887 GACACCACTTGAAGGCGCGCTCTGCGGACACGCGCTCTGACGCGCAGAGCTCC 1828  
 QY 115 AGGCGCGGACAGGAAGGCGGACGCGCTTCCAGAGGCGCGCGCGCAGAGAAAGTT 174  
 DB 1827 TGCTCCGTGGGGTAGATGATGCGCGCTTGACACATGACGTGCGCTGCTGAGAGCC 1768  
 QY 175 GCGCCAGGCGACGCGCGCTGAGCGAGCGGAGCGGCTTCTCAAGAGCGCG----GGCGA 229  
 DB 1767 GCGCCGCGCGCGCGCGCTGAGCGGCGCGCTGCGCGGCTGAGCTGCGCTGAGAGAGA 1708  
 QY 230 GCGCCGCGCGCTGAGCGGCGGAGCGCGGTATTAAGAGCGCTGCGCTTGGCCGCGAGC 289  
 DB 1707 GCGTGGGCGCAGTGGGCGGCGCGCTGCGGCGGACAGTCTGCGGGTGGCTCTCTCCAGC 1648  
 QY 290 GCGAGGTTCCCGCGCGCGC 308  
 DB 1647 CGCTCTCTCTCGCGCTGCC 1629  
 RESULT 40  
 AAK51993/C  
 ID AAK51993 standard; cDNA, 4809 BP.  
 XX  
 AC AAK51993;  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polynucleotide SEQ ID NO 538.  
 XX  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorder; arthritis; inflammation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157190-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001WO-US04098.  
 XX  
 PR 03-FEB-2000; 2000US-0496914.  
 PR 27-APR-2000; 2000US-0568975.  
 PR 20-JUN-2000; 2000US-0598075.  
 PR 19-JUL-2000; 2000US-0628025.  
 PR 01-SEP-2000; 2000US-0654936.  
 PR 15-SEP-2000; 2000US-0663561.  
 PR 20-OCT-2000; 2000US-0693325.  
 PR 30-NOV-2000; 2000US-0728422.  
 XX  
 PA (HSE-) HXSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y,  
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW,  
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
 XX

DR WPI; 2001-476283/51.  
 DR P-PSDB; AAK78860.  
 XX  
 PT Nucleic acids encoding polypeptides with cytokine-like activities,  
 PT useful in diagnosis and gene therapy -  
 XX  
 PS Claim 1; Page 1939-1944; 6221pp; English.  
 XX  
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the  
 CC encoded polypeptides (AAK78823-AAK80020) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
 CC (AAK80020) are omitted as the relevant pages from the sequence listing  
 CC were missing at the time of publication.  
 XX  
 SQ Sequence 4809 BP; 955 A; 1595 C; 1467 G; 792 T; 0 other;  
 Query Match 13.6%; Score 43.8; DB 22; Length 4809;  
 Best Local Similarity 51.0%; Pred. No. 1.7;  
 Matches 132; Conservative 0; Mismatches 122; Indels 5; Gaps 1;  
 QY 55 GACAAAGGCGGCGCTGCTCTCTCAAGAGGCGCCAGCGCTTCCAGAGAAAGTCTTCG 114  
 DB 1938 GACACCACTTGAAGGCGCGCTGCTGCTGAGACACGCGCTTGCAGCGCCAGAGCTTC 1879  
 QY 115 AGGCGCGGACAGGAAGGCGGACGCGCTTCCAGAGGCGCGCGCGCGCAGAGAAAGTT 174  
 DB 1878 TGCTCCGTGGGGTAGATGATGCGCGCTTGACACATGACGTGCGCTGCTGAGAGCC 1819  
 QY 175 GCGCCAGGCGACGCGCGCTGAGCGGAGCGGCGGCGGCTTCTCAAGAGCGCG----GGCGA 229  
 DB 1818 GCGCGCGCGCGCGCGCTGAGCGGCGGCGGCGGCTGCGCGGCTGAGAGAGAGA 1759  
 QY 230 GCGCGCGCTGAGAGGCGGACGCGGTATTAAGAGCGCTGCGCTTGGCCGCGAGC 289  
 DB 1758 GCGTGGGCGCAGTGGGCGGCGCGCGCTGCGGCGGACAGTCTGAGGCTCTCTCCAGC 1699  
 QY 290 GCGAGGTTCCCGCGCGCGC 308  
 DB 1698 CGCTCTCTCTCGCGCTGCC 1680

Search completed: November 6, 2003, 07:07:42  
 Job time: 242.409 secs

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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 4; Length 570;  
Best Local Similarity 100.0%; Pred. No. 9e-03; Indels 0; Gaps 0;  
Matches 78; Conservative 0; Mismatches 0

QY 246 GCGAGACCGCGTATTAAGAGCTCTGCTGCTTCCCGGCGACCGCGAGTTCCCGCGCG 305  
DB 1 GCGAGACCGCGGATTAAGAGCTCTGCTGCTTCCCGGCGACCGCGAGTTCCCGCGCG 60

QY 306 GCGCGGAGCGCGCGCGCGCG 323  
DB 61 GCGCGGAGCGCGCGCGCGCG 78

## RESULT 2

US-08-586-165-8/c  
Sequence 8, Application US/08586165  
Patent No. 6054298

## GENERAL INFORMATION:

APPLICANT: Laufer, Edward M.  
APPLICANT: Orozco, Olivia E.  
APPLICANT: Tabin, Clifford J.  
TITLE OF INVENTION: F-tinge Proteins and Pattern Formation  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02173

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/586,165  
FILING DATE: 16-JAN-1996  
CLASSIFICATION: 800

## ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: HU95-05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-9540  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3937 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

US-08-586-165-8

Query Match 14.1%; Score 45.4; DB 3; Length 3937;  
Best Local Similarity 51.4%; Pred. No. 0.095; Indels 2; Gaps 1;  
Matches 130; Conservative 0; Mismatches 121

QY 63 CCGGCGCTGCTCTCTCAAGAGGCGCCCAAGCGCTTCCCAAGAGAAAGTCTTCAAGGCGCG 122  
DB 371 CCGGCGACGCTCTCTCCCGCGCGCGCGCTTCCCGCTTCCGAGAGGCGCTGCTGCGCG 312  
QY 123 GCAG-GGAAGGAGGACCGGCTTCCCAAGGCGCGCGCGCGCGACAGAAAGTTGCGAG 180  
DB 311 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTTCCCGCGCGAGCAGCAG 252

QY 181 GGCACGCGCTGTAGCGAGCGGCGAGGCTTCTCAAGAGCGCGCGAGCGCGCGCTG 240  
DB 251 GAGAACGCGCGCGCGCGGAGCGGACAGAGAAACAGCTTGTGAGAGCGCCCAAGCGAGA 192  
QY 241 GAGGCGGAGGACCGGATTAAGAGCTCTGCTGCTTCCCGGCGAGCGCGAGTTCC 300  
DB 191 GTGCTCATGTGTGGCGCGCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCTCATGTGCGCC 132  
QY 301 GCGCGCGCGCGAG 313  
DB 131 GCGAGCGCGCGCG 119

## RESULT 3

US-08-232-463-14/c  
Sequence 14, Application US/08232463  
Patent No. 5670367

## GENERAL INFORMATION:

APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/935,313  
FILING DATE: 26-AUG-1991  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-9300  
TELEFAX: (703) 683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: PTZ9pt-Fis

US-08-232-463-14

Query Match 13.5%; Score 43.6; DB 1; Length 7218;  
Best Local Similarity 4.5%; Pred. No. 0.24; Indels 0; Gaps 0;  
Matches 13; Conservative 162; Mismatches 111

QY 7 GGGGTACAGCCGGAAGCAAGTGTGCGGCGCGGCGGCTTCCGCGAGACAAGGCGCG 66  
DB 1327 RRR 1268  
QY 67 GCGTCTCTCTCAAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 126

[illegible]

RESULT 4  
 US-08-572-951-1/c  
 Sequence 1, Application us/08572951  
 Patent No. 5824790  
 GENERAL INFORMATION:  
 APPLICANT: KEELING, PETER L.  
 APPLICANT: KNIGHT, MARY E.  
 APPLICANT: GUAN, HANPING  
 TITLE OF INVENTION: MODIFICATION OF STARCH  
 TITLE OF INVENTION: SYNTHESIS IN PLANTS  
 NUMBER OF SEQUENCES: 41  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CUSHMAN DABRY & CUSHMAN  
 ADDRESSEE: Intellectual Property Group of  
 ADDRESSEE: Pillsbury Madison & Suto LLP  
 STREET: 1100 New York Avenue, N.W.  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3918  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/572,951  
 FILING DATE: 15-DEC-1995  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/346,602  
 FILING DATE: 29-NOV-1994  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/263,921  
 FILING DATE: 21-JUN-1994  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Paul N. Kokula  
 REGISTRATION NUMBER: 16,773  
 REFERENCE/DOCKET NUMBER: 222957/1.02.15C  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 861-3000  
 TELEFAX: (202) 822-0944  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2990 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-572-951-1

Query Match	13.4%	Score 43.4;	DB 1;	Length 2990;
Best Local Similarity	49.3%;	Pred. No. 0.25;		
Matches 113;	Conservative 0;	Mismatches 110;	Indels 0;	Gaps 0;
24	CGAAGTCCGGGCGGGGCTCGGGGAGACAAAGCCGGGCTCTCTCAAG	83		

Db	813	CGGGGGGGGAGGAACCGGGGCACGAGGGGGGGCCGACGACCGGGTGGCAGCGGGCG	75
QY	84	GGGCCCCAGCGGCTTGGCCMAAGGAAGTCTCTCAAGGCCCGGGCAAGGAAGGGGGCA	14
Db	753	CGGCGCGGGGCGCTCTCTCTGCTCAGCTCCGCAAGCAACGGGCGGGCGACACGCCCTGAG	694
QY	144	TCCAGAGGCGCCGCGGCGCAGCAGGAAGTTGGCCAGGGCA	203
Db	693	CTTCGCGGGCGGCGCCCGGTGCGCAGCGGGCGCGCAGGCGCCCGCGCAGAGGAGG	634
QY	204	CAGGGCTTTCTCAGAGACGCGGGCCAGGCGGGCGCTGAGAGGGGGAGGA	252
Db	633	CAGCGGCGCCACGCGCCAGGGCGCTGCGCATTTGGAGAGAGAGAGCA	585

```

RESULT 5
US-09-128-155-16/c
; Sequence 16, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PaetSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 15231
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(15231)
OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

```

[illegible]

RESULT 6  
US-08-031-538-10/c  
; Sequence 10, Application US/08031538  
; Patent No. 5968817  
; GENERAL INFORMATION:



```

APPLICANT: Sutcliffe, J Gregor
APPLICANT: Eklender, Mark G
APPLICANT: Lovenberg, Timothy W
TITLE OF INVENTION: HUMAN SEROTONIN RECEPTORS, DNA ENCODING
TITLE OF INVENTION: THE RECEPTORS, AND USES THEREOF
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESSES:
ADDRESSES: The Scripps Research Institute, Office of
ADDRESSES: Patent Counsel
STREET: 10666 No. 5968817th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,538
FILING DATE: 19930315
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSP5099P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2040 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-031-538-10

Query Match 12.8%; Score 41.4; DB 2; Length 2040;
Best Local Similarity 49.8%; Pred. No. 0.67; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 106;

QY 28 GGTGCGGGCCGGGGTGGGCTTCGCGGAGACAAAGCCGGGCTTCTCTCAGAGGGCC 87
DB 566 GGGGCTGGCCACTGGGGGGCGCCGCTCGGCTCGGAGACCCCGCAGCTCCAGAGGTCCC 507
QY 88 CCAAGCGCTGCGCAAGAGAGAGTCTCGAGGCCCGGGGAGGAGGGGCAACGGGCTTCCC 147
DB 506 CCAAGCTCTGCGATGACGCGTGGGGGAGACTCCCGCGGGAGGACCAAGCGGTCCC 447
QY 148 AGGGCCCGCGCGCGCAGCAGAGATTGGCCAGGGCAGCGCCGTGAGCGAGCGGGCAGG 207
DB 446 ACGGCGACGCGAGAGAGAGCGAGGTGGGCGAGCCGAGCTGGCGGTGGCCGACCGCAG 387
QY 208 GCTTCTCAGAGCGCGGGGCGAGCGCGCGC 238
DB 386 CCGCGACGATCGCCCGCGGGCGCGGAGC 356

RESULT 7
US-09-602-877A-78/c
Sequence 78, Application US/09602877A
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.446CS

```

```

CURRENT APPLICATION NUMBER: US/09/602,877A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 78
LENGTH: 1574
TYPE: DNA
ORGANISM: Homo sapiens
US-09-602-877A-78.

Query Match 12.5%; Score 40.4; DB 4; Length 1574;
Best Local Similarity 45.8%; Pred. No. 1.1;
Matches 140; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 17 CGCAAGGAGAGGTGCGGGCGCGGGGTGGCTTCGCGGAGACAAAGGCCGGGCTGCTCT 76
DB 351 CGCAGCGCGCTGGGGGAGACCCGAGACCGGAGTTGAAGAGTGAAGCGCCGCGCGCC 292
QY 77 CTCAGAGGCGCCCGAGGCGCTGCGCAAGAGAGTCTCTGAGGCCCGGGCAGGAGGGGCG 136
DB 291 TCCTCAGAGAGCTTCGCGGGAGCCCGACATCTGAGGCTGCCAGGGTCTGCGGGTCC 232
QY 137 ACGGCTTCCAGGGCCCGCGCGCCGCGCAGCAGAAAGTTGGCCAGGGCAACGGCCGTGAGCG 196
DB 231 CGGACCCCGCGGGCGCGCAGACCGGGCGAGCAACAGAGAGCGAGACCGGGCG 172
QY 197 GAGCGGGAGAGGCTTCTCAGAGAGCGGCGAGGCGCGCTGAGGGCGAGAGACCG 256
DB 171 GTGGGGCGGGGCCCCCTGGGCCCCGAGCAGAGAGGGGACACCGTTGCGGGGCTCG 112
QY 257 GATTAAGAGCTTCGTGCGCTTGCAGCGGAGCCGAGAGTTCCCGCGCGCCGAGGCC 316
DB 111 ATGAGCGCAGAGAAAGTTGCTCGGACCCGACCGAGACAGAGAGGCTCGAGAGCGGAGTCCG 52
QY 317 CCGCGC 322
DB 51 GCGCTC 46

RESULT 8
US-08-836-329-1/c
Sequence 1, Application US/08836329
Patent No. 6090546
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method for the Detection of Ras Oncogenes,
TITLE OF INVENTION: In Particular the K-Ras Oncogene
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,329
FILING DATE:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 825..947
FEATURE:
NAME/KEY: exon
LOCATION: 1388..1567
FEATURE:
NAME/KEY: exon

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QY 108 GTCTCTGAGGACCCGGGCAAGGGAAAGGGGGGACACGGGCTTCCACAGGGCCGGCCGACAGCA 167

QY	168	GGAAGTTGGCCAGAGGCAAGCGGCGGTGAGCGAGAGCGGCGAGGGCTTTCTCAGAGAGCGCGGAC	227
Db	12511	GTCCGGAAGGCTATCACACGCGGCCACAGCGGGTGTGTGGCGTCCGACACGAGGCC	12452
QY	228	GAGCGCGGCGCTGAGAGGGGAGAGACCGGGTATTAAAGCCTTCGTGCGCTTCGCGGGCA	287
Db	12451	GCGGTTGTCCACCGCGGTTGTCCGCGCGGAGCGCTCCAGCAGTACGAGTGTGCGCGCGAA	12392
QY	288	GCGGAGGTTCCCGCGCGCGCCCGAGCGCCCGCG	321
Db	12391	GGAATACGTGAGGACGATCCACGCGGTGCGCCCG	12358
RESULT 12			
US-09-320-878-19/c			
Sequence 19, Application US/09320878A			
Patent No. 6117659			
GENERAL INFORMATION:			
APPLICANT: ASHLEY, Gary			
APPLICANT: BETLACH, Melanie C.			
APPLICANT: BETLACH, Mary C.			
APPLICANT: MCDANIEL, Robert			
APPLICANT: TANG, Li			
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE			
FILE REFERENCE: 300622002120			
CURRENT APPLICATION NUMBER: US/09/320,878A			
CURRENT FILING DATE: 1999-05-27			
EARLIER APPLICATION NUMBER: CIP OF 09/141,908			
EARLIER FILING DATE: 1998-08-28			
EARLIER APPLICATION NUMBER: CIP OF 09/073,538			
EARLIER FILING DATE: 1998-05-06			
EARLIER APPLICATION NUMBER: CIP OF 08/846,247			
EARLIER FILING DATE: 1997-04-30			
EARLIER APPLICATION NUMBER: 60/119,139			
EARLIER FILING DATE: 1998-02-08			
EARLIER APPLICATION NUMBER: 60/100,880			
EARLIER FILING DATE: 1998-09-22			
EARLIER APPLICATION NUMBER: 60/087,080			
EARLIER FILING DATE: 1998-05-28			
NUMBER OF SEQ ID NOS: 34			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO 19			
LENGTH: 38506			
TYPE: DNA			
ORGANISM: Streptomyces venezuelae			
US-09-320-878-19			
Query Match 12.3%, Score 39.6; DB 3; Length 38506;			
Best Local Similarity 49.1%; Pred. No. 1.8;			
Matches 105; Conservative 0; Mismatches 109; Indels 0; Gaps 0;			
QY	108	GTCTCCGAGGCGCGCGGAGGAGAGGGGAGCAGGGCTTCCAGAGGCGCGCGCGAGAGA	167
Db	10713	GTCCGCGAGCGACCGGAGTGGGTGCCAGAGGAGCGCGCTCGTAGCAGCGCGTCCCG	10654
QY	168	GGAAGTTGGCCAGAGGCAAGCGGCGGTGAGCGAGCGGAGAGGCTTTCTCAGAGAGCGCGGC	227
Db	10653	GTCCGGAAGGCTGACACAGCGCGCGGAGAGGCGGTGTGCGCGGTCCAGACCGAGGCC	10594
QY	228	GAGCGCGGCGCTGAGAGGGGAGAGACCGGGTATTAAAGCCTTCGTGCGCTTCGCGGGCA	287
Db	10533	GCGGTTGTCCACCGCGGTTGTCCGCGCGGAGCGCTCCAGCAGTACGAGTGTGCGCGCGAA	10532
QY	288	GCGGAGGTTCCCGCGCGCGCCCGAGCGCCCGCG	321
Db	10533	GGAATACGTGAGGACGATCCACGCGGTGCGCCCG	10500
RESULT 13			
US-09-141-908-1/c			
Sequence 1, Application US/09141908			
Patent No. 6503741			

```

GENERAL INFORMATION:
APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: Combinatorial polypeptide libraries Produced Using a
File REFERENCE: 300622002100
CURRENT APPLICATION NUMBER: US/09/141,908
CURRENT FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: PROV. 60/076,919
EARLIER FILING DATE: 1998-03-05
EARLIER APPLICATION NUMBER: PROV. 60/087,080
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 38506
TYPE: DNA
ORGANISM: Streptomyces venezuelae
US-09-141-908-1

Query Match 12.3%; Score 39.6; DB 4; Length 38506;
Best Local Similarity 49.1%; Pred. No.1.8;
Matches 105; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 108 GTCTCGAGGCGCGGCGAGGAGGAGGCGGCGCTTCCAGAGGCCCGCGCGCAGCA 167
DB 10713 GTCCGCGAGCGCAGGGGCGGTGCGCAGGAGAGGCGCGCGGTGACAGCAGGCGCGCCG 10554
QY 168 GGAAGTTGGCCAGGCGCGCGCGCGTGAAGCGGAGCGGCGCAGGGCTTTCTCAGAGAGCGCGGCG 227
DB 10653 GTCCGGAAGCTACACACCGCGCGCGCAGCAGCGGGTGTGTGCGGGTGTCCAGACCGAGCGCC 10594
QY 228 GAGCGCGCGCGCTGAGGAGCGGAGAGACCGGTTATAGAAACCTTCGTGCGCTTGCAGCGGCGCA 287
DB 10593 GCGCGTGTCCACCGCGGCGGTGCGCGCGCGCGCGCTCCAGCGACGTAGCGGTGCGCGCGAA 10534
QY 288 GCGCGAGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 321
DB 10533 GGAAGTACGTGGGCGAGGTCCACGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 10500

RESULT 14
US-09-657-440-19/c
; Sequence 19, Application US/09657440
; Patent No. 6509455
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYPEPTIDE SYNTHASE
; FILE REFERENCE: 300622002120
; CURRENT APPLICATION NUMBER: US/09/657,440
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 09/320,878
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: CIP OF 09/141,908
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 38506
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-657-440-19

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QY 152 CCCGCGCGCGCGAGAGAGAAATTGGCCAGAGGCAAGCGCCCTGAGCGAGCGGCGAGGGCTT 211  
DB 7333 GCAGGCGAGCGCTGCGAGGTCGCGGAGCGCCAGCGCGCGCTGCTCGGGCGG 7274

QY 212 TCTCAGAGAGCGGCGGCGAGCGCGCTGAGAGGCGGAGACCGGG 257  
DB 7273 CCCCAGAGACCGGCGGAGGTGATGTCAACCGCGCGGAGAGGTGCGGG 7228

RESULT 17  
PCT-US91-06532-1/C  
Sequence 1, Application PC/TUS9106532  
GENERAL INFORMATION:  
APPLICANT: Kozlman, Bernard  
TITLE OF INVENTION: Recombinant Herpes Simplex Viruses  
TITLE OF INVENTION: Vaccines and Methods  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: Two First National Plaza Suite 2100  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 19910910  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Gruber, Lewis S.  
REGISTRATION NUMBER: 30,060  
REFERENCE/DOCKET NUMBER: 27373/8235  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/346-5750  
TELEFAX: 312/984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1335 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US91-06532-1

Query Match 12.0%; Score 38.6; DB 5; Length 1335;  
Best Local Similarity 48.1%; Pred. No. 2.6;  
Matches 139; Conservative 0; Mismatches 149; Indels 1; Gaps 1;

QY 4 CGTGGGATCAAGACCGCAAGAGGAGGCGGCGGCGGCTTCCGCGAGACAAAGGC 63  
DB 660 CGCGGGGTGTCGCGGGGTGCGGGGGTTCGCGGGGGTTCGCGGGGGCTCCGG 601

QY 64 CGGGCTGCTCTCTCAGAGGCGCCCAAGCGCTGCGCAAGAGAGTCTCGAGCGCGGG 123  
DB 600 CGCCCTCTCCCGCCCGCGCTCGCAGGCGCGGCGGCAAGGTCTCTCGGGTGAACG 541

QY 124 CAGGAAAGGCGGCGCGCTTCCAGAGCGCGCGCGCGCGGAGAGAAATTGGCCAGGGC 183  
DB 540 CAGGCGAGGCGGCGGCGCGCGGAGGCGGAGGCGGTGAGGCGGGGTGGAGGGGTT 481

QY 184 ACGGCGGTGAGCGGAGCGGCGGAGGCGCTTCTCAGAGAGCGCGCGGAGGC- CGGCGCTGGA 242  
DB 480 AGCCCGCGCCCTCGGCGCGCGCGCGGCGGTGAGGACCGGAGGCGGCGGCGGT 421

QY 243 GGGGCGAGGACCGGCTATTAAGAGCCTTGCGCTTGGCGGAGCGCG 291

DB 420 GGGCGGGGCTCTGCGCGCGCGCTCGGCGGAGGAGCTGTCCGCGCAATGCG 372

RESULT 18  
US-08-398-008A-1  
Sequence 1, Application US/08398008A  
Patent No. 5665588  
GENERAL INFORMATION:  
APPLICANT: Kornbluth, Jacki  
TITLE OF INVENTION: DNA Encoding Natural Killer Lytic Associated  
TITLE OF INVENTION: Protein  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gilbreth & Adler, P.C.  
STREET: 8011 Candle Lane  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage  
COMPUTER: MACINTOSH Plus  
OPERATING SYSTEM: Macintosh  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA:  
FILING DATE: March 2, 1995  
APPLICATION NUMBER: US/08/398,008A  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/126,501  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Dr. Benjamin Aaron  
REGISTRATION NUMBER: 35,423  
REFERENCE/DOCKET NUMBER: B5705CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 777-2321  
TELEFAX: (713) 777-6908  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2823 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double-stranded  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: no  
AMBI-SENSE: no  
US-08-398-008A-1

Query Match 12.0%; Score 38.6; DB 1; Length 2823;  
Best Local Similarity 47.8%; Pred. No. 2.7; Indels 1; Gaps 1;  
Matches 142; Conservative 0; Mismatches 154;

QY 28 GGTGCGGGCGCGGGGTGCGGCTTCCGCGAGACAAAGGCGCGGCTTCTCTCAGAGGGCC 87  
DB 335 GGGCCAAAGCGCGAGGCGGCGCGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCG 394

QY 88 CCAGCGCTGCGCAAGAGAGATCTCAGAGGCGCGCGCGCGCGCGGAGAGGCGGCGCTTCC 147  
DB 395 CTGCGCGCGCGCGAGGCGCGCGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCG 454

QY 148 AGGCGCGCGCGCGCGCGAGAGAGTTGGCCAGGCGCAAGCGCGTGAAGCGAGCGGCGAG 207  
DB 455 AGGCGAGGCGCGCGCGCGCGCGGCGGCGGAGCGCTGGGTTGAGAGTGAAGGCGCGGAG 514

QY 208 GCTTCTCAGAGCGCGCGCGCGAGCGCG- GCGCTGAGGAGCGAGGACCGGGTATTAAGAG 266  
DB 515 GCGGTGCGCGCGCGCGGAGGAGAGGTGAGGTGCGCTGAGCTGAGTGGCGGCTGCGCGCTG 574

QY 267 CCTGCGGCTTGGCGCGCGCGCGAGGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGC 323

Db 575 AGCGGGCCCCGCGCTCTCTCAGCTGTCCGACCGCTTCGCGGAGACTGCTCCGCC 631

RESULT 19

US-08-893-333-1

Sequence 1, Application US/08893333A

Patent No. 5981705

GENERAL INFORMATION:

APPLICANT: Kornbluth, Jacki

TITLE OF INVENTION: DNA Encoding Natural Killer Lytic Associated Protein

FILE REFERENCE: D5705CIP/D

CURRENT APPLICATION NUMBER: US/08/893,333A

CURRENT FILING DATE: 1997-07-16

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 1

LENGTH: 2823

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

LOCATION: 190..1953

OTHER INFORMATION: CDS

US-08-893-333-1

Query Match 12.0%; Score 38.6; DB 2; Length 2823;

Best Local Similarity 47.8%; Pred. No. 2.7;

Matches 142; Conservative 0; Mismatches 154; Indels 1; Gaps 1;

QY 28 GGGGCGGCGCGGGGCTGGGCGCTGCGGAGCAAGAGCGCGGCGCTCTCTCAGAGGGCC 87

Db 335 GGGCCAGGCTGACAGCGCCGAGCGCCGCCCGCGCTGCGCGCGCGCGCGCGCGCGCC 394

QY 88 CCAGCGCCTGCAAGAGGAAGTCTCTGAGGCGCGCGCGAGGAGGAGGAGCGGCTTCCC 147

Db 395 CTGCGCGGCGCCAGGCG 454

QY 148 AGGCG 207

Db 455 AGCGGAGGCG 514

QY 208 GCTTCTCAGAGAGCG 266

Db 515 GCGGTGCG 574

QY 267 CCTGTGCGCTTGGCG 323

Db 575 AGCGGGCCCCGCGCTCTCTCAGCTGTCCGACCGCTTCGCGGAGACTGCTCCGCC 631

RESULT 20

US-09-593-589-3

Sequence 3, Application US/09593589

Patent No. 6306655

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Madeline M. Butler

APPLICANT: Jacqueline Wyatt

TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP ALPHA EXPRESSION

FILE REFERENCE: RTS-0119

CURRENT APPLICATION NUMBER: US/09/593,589

CURRENT FILING DATE: 2000-06-13

NUMBER OF SEQ ID NOS: 94

SEQ ID NO 3

LENGTH: 3318

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (592) ... (1668)

US-09-593-589-3

Query Match 11.9%; Score 38.4; DB 4; Length 3318;

Best Local Similarity 47.5%; Pred. No. 3;

Matches 114; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 83 GGGCCCCAGCGCGCTGCAAGAGGAAGTCTCTCAGAGCGCGCGCGAGGAGGAGCGAGCG 142

Db 136 GGGCTTCCGCGCGCTGCTGGAATACGGGCGCTTACGAGGAGCGAGAGAGGAGCGCGCG 195

QY 143 TTCCAGAGGCGCGCGCGCGCGCGCGAGAGGAATTGCGCAGGAGCAAGCGCTGAGCGAGCG 202

Db 196 TACGACACAGTGTGGCG 255

QY 203 GCAGGCTTCTCAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 262

Db 256 CGCGGCTGTGCTGGCGCGCGCTGAGAGCGGTGGCGCTTGGCGCGCGCGCTGCTGGAGCG 315

QY 263 GAAGCTGTGCGCTTGGCGCGCGCGCGCGCGAGGTTCCCGCGCGCGCGCGCGCGCGCG 322

Db 316 GCGGCGCTGTGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 375

## RESULT 21

US-08-814-095-7/C

Sequence 7, Application US/08814095

Patent No. 6025183

## GENERAL INFORMATION:

APPLICANT: Soreq, Hermona

APPLICANT: Zakut, Haim

APPLICANT: Shani, Moshe

TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR

TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTRATES

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: KOHN & ASSOCIATES

STREET: 30500 No. 6025183Western Highway, Suite 410

CITY: Farmington Hills

STATE: Michigan

COUNTRY: U.S.

ZIP: 48334

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/814,095

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Montgometry, Ilene N.

REGISTRATION NUMBER: 38,972

REFERENCE/DOCKET NUMBER: 2391,00066

TELECOMMUNICATION INFORMATION:

TELEPHONE: (248) 539-5050

TELEFAX: (248) 539-5055

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 35060 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "Cosmid including ACHÉ

DESCRIPTION: Promotor, ACHÉ gene and ARS gene"

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

POSITION IN GENOME:

CHROMOSOME/SEGMENT: 7q22

FEATURE:

NAME/KEY: Promoter

LOCATION: 4089..22464

OTHER INFORMATION: /function= "ACHÉ Promotor"

OTHER INFORMATION: /standard\_name= "ACHÉ Promotor"

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NAME/KEY: exon
LOCATION: 22465..22537
OTHER INFORMATION: /function= "non-translated"
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 1
FEATURE:
NAME/KEY: exon
LOCATION: 24090..25177
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "(translation start:
OTHER INFORMATION: 24110)"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 2
FEATURE:
NAME/KEY: exon
LOCATION: 25524..26009
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 3
FEATURE:
NAME/KEY: exon
LOCATION: 27005..27274
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 4
FEATURE:
NAME/KEY: exon
LOCATION: 27255..28007
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 5
FEATURE:
NAME/KEY: terminator
LOCATION: 27385..27387
FEATURE:
NAME/KEY: exon
LOCATION: 28008..28129
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 6
FEATURE:
NAME/KEY: terminator
LOCATION: 28129..28131
FEATURE:
NAME/KEY: exon
LOCATION: 34528..34895
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "arsenite resistance
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 1
FEATURE:
NAME/KEY: exon
LOCATION: 34092..34358
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 2
FEATURE:
NAME/KEY: exon
LOCATION: 33779..33963
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
FEATURE:
NAME/KEY: exon
LOCATION: 33493..33591
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 4
FEATURE:
NAME/KEY: exon
LOCATION: 33297..33408
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 5
OTHER INFORMATION: /gene= "AR"
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OTHER INFORMATION: /gene= "AR"
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 11
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
OTHER INFORMATION: /gene= "ARS"
OTHER INFORMATION: /number= 16
US-08-814-095-7
Query Match 11.9%; Score 38.4; DB 3; Length 35060;
Best Local Similarity 47.7%; Pred. No. 3.2;
Matches 143; Conservative 0; Mismatches 156; Indels 1; Gaps 1;
QY 23 GCGAAGTGGGCGGCGGCTCGCGAGACAAAGCCGCGCTCTCTCAGA 82
Db 22726 GCGTGGGCGTGGTGAAGGCGCGGGAAGATTCCGAGCGAGTGGCGGCGAGC 22667
QY 83 GGGCCCGAGGCGCTGCGAGAGAGATCTCGAGGCGCGGAGGAGGAGCGAGC 142
Db 22666 GAGAGCGCGCGCGGCGAGGCGCGGAGAGCGGAGCGCTCCGTTAGGCGGCGCTGAGC 22607
QY 143 TTCCAGGCGCGCGCGCGCGAGAGATTGGCCAGGCGACGCGCGTGAAGCGAGCGG 202

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Db 22606 CCCTCGGGAGCCGACGGTGCCCCCGGACCTTAAAGAGATGCCGGCGGGAGG 22547  
QY 203 GCAGGGCTTTCTAGAGAGCGCGGGCGAGCGCGGCTGAGGGGCGAGACCGGTTATA 262  
Db 22546 G-AGACTCAGCTAGGGCGGCGGAGCGCGGCGCGCGCGCGCGGCGGCGGCGG 22488  
QY 263 GAAGCTCGTGGCTTGGCGGCGAGCGCGAGGTTCCCGCGCGCGCGCGCGCGCG 322  
Db 22487 GCCGATGTTCCCGCGGCGAGAGCTGAGCGGAGCTGACAGCGCGCGCTCGCGCGCG 22428

RESULT 22  
US-08-781-802-7  
; Sequence 7, Application US/08781802  
; Patent No. 5969121  
; GENERAL INFORMATION:  
; APPLICANT: ALLEN, Larry  
; APPLICANT: AIKENS, John  
; APPLICANT: FONSTEIN, Michael  
; APPLICANT: VONSTEIN, Veronika  
; APPLICANT: DEMIRJIAN, David  
; APPLICANT: CASADABAN, Malcolm  
; TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 S. Wacker Drive 32nd Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781,802  
FILING DATE: 10-JAN-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/019,580  
FILING DATE: 12-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/009,704  
FILING DATE: 11-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/001,995  
FILING DATE: 01-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Chao, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 95,963-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3147 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 245..1231  
OTHER INFORMATION: /note="TspA E101 sequence longest  
open reading frame; other possible start codons are TTG/leu9;  
TTG/leu13; TTG/leu15; GTG/val43"

; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 245..1231  
US-08-781-802-7

Query Match 11.8%; Score 38.2; DB 2; Length 3147;  
Best Local Similarity 47.8%; Pred. No. 3.3;  
Matches 141; Conservative 0; Mismatches 153; Indels 1; Gaps 1;

QY 25 GAAGTGGCGGCGCGGGGTGGGCTTCGCGAGCAAAAGCGGGGCTGCTCTCTAGAG 84  
Db 2386 GGAGGCGCTGAGGAGGCGGCGCGCGCTGGCGCGGAGGAGTGAGACCGCTCAAGG 2445  
QY 85 GCCCAGCGCCT-GCCAAGAGAGTCTCGAGCGCCGCGGCGAGGAAGGGGCGAGCGCT 143  
Db 2446 GTGGCTGGCGCTTGGAGGCGGGAAGCGAGAGCGCGGCTTCCAGCGCGCGG 2505  
QY 144 TCCAGAGGCGCGCGCGCGCGAGCAAGATTGGCCAGAGGCAAGCGCTGAGCGGAGCGG 203  
Db 2506 CATCTACTCGGCGCTTCCCAAGAGCGCCCTCTGAGGCGCTTGGAGGCGG 2565  
QY 204 CAGGCTTTCTAGAGAGCGCGGCGAGCGCGCGCTGAGGGCGAGACCGGTTATAAG 263  
Db 2566 CGCTCTTCCAGAGGCGCTTGGCGCGGCGAGCGGCGGAGGCGGCGGCGGCGG 2625  
QY 264 AAGCTCGTGGCTTGGCGCGGCGAGCGAGGTTCCCGCGCGCGCGCGCGCGG 318  
Db 2626 CCTCTTAAGGGGCTTCTTCTCTGCGCCAGAGACCGCGGAGGCGCTGGCGCG 2680

RESULT 23  
US-08-694-078-7  
; Sequence 7, Application US/08694078  
; Patent No. 6218163  
; GENERAL INFORMATION:  
; APPLICANT: ALLEN, Larry  
; APPLICANT: AIKENS, John  
; APPLICANT: FONSTEIN, Michael  
; APPLICANT: VONSTEIN, Veronika  
; APPLICANT: DEMIRJIAN, David  
; APPLICANT: CASADABAN, Malcolm  
; TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff, Ltd.  
; STREET: 300 S. Wacker Drive 7th Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/694,078  
FILING DATE: 07-AUG-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/019,580  
FILING DATE: 12-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/009,704  
FILING DATE: 10-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/001,995  
FILING DATE: 07-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Chao, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 95,963-C  
TELECOMMUNICATION INFORMATION:



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TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3147 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 245..1231
OTHER INFORMATION: /note= "TSP4_E101 sequence longest
open reading frame; other possible start codons are TTG/Leu9
OTHER INFORMATION: TTG/Leu13; TTG/Leu15; GTG/Val43"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 245..1231
US-08-694-078-7

Query Match      11.8%; Score 38.2; DB 3; Length 3147;
Best Local Similarity 47.8%; Pred. No. 3.3; Mismatches 153; Indels 1; Gaps 1;
Matches 141; Conservative 0;

25 GAAGGTGGCGGCCTGGGCTTCGCCAGACAAAGCCCGGCTTGCTCTTCAGAG 84
2386 GGAGGCTCTGAGGGGGCGGCCCGCTGGGCGGGCGGTGAGCGGCTTAAGG 2445
85 GCCCAGAGGCTT-GCCAGAGAGAATCTTCAGAGCCCGGCGAGGAAGGGGCAAGGCT 143
2446 GTGGCTGGCCCTTCGAGAGGGGGAAAAGCCGAGAGAGGCCCGGGCGCTTCCAAGCGCGGAC 2505
144 TCCGAGGGCCCCCGCGCGCGAGAGAGATTGGCCAGGCGCAAGCGCGTAGAGCGAGCGG 203
DB CATCTACTCGGACCCTTCCCAAGACGCCCTCCTCTGGGCTTCGGGGCTTTGGAGAGCGGG 2565
OY 204 CAGGCGCTTTCTAGAGAGCGCGGGCGAGCGCGCGCTGAGAGGGGCGAGAACCGGGATAG 263
DB 2566 CGGCTCTTCCGAGAGAGCCCTGAGCCCGGCGAGAGCGGGCGAGAGCGGGCGGAGCGGC 2625
OY 264 AAGCCTCGTGCCTTCCCGGAGCGGAGGTTCCCGCGCGCCCTCGAGCCCCC 318
DB 2626 CCTCCTTAAGGGGCTTCTCTCTGCGCCAGAGCCCGGCGAGGCGCTTGAGCGCC 2680

RESULT 24
US-09-058-260-7
; Sequence 7, Application US/09058260B
; Patent No. 6218167
; GENERAL INFORMATION:
; APPLICANT: Allen, Larry
; APPLICANT: Atkins, John
; APPLICANT: Fongstein, Michael
; APPLICANT: Vonstein, Veronika
; APPLICANT: Demitjian, David
; APPLICANT: Casadaban, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
FILE REFERENCE: 95-963-H
CURRENT APPLICATION NUMBER: US/09/058,260B
EARLIER PILING DATE: 1993-04-10
EARLIER APPLICATION NUMBER: 60/001, 995
EARLIER PILING DATE: 1996-08-07
EARLIER APPLICATION NUMBER: 60/009, 704
EARLIER PILING DATE: 1996-01-11
EARLIER APPLICATION NUMBER: 60/019, 580
EARLIER PILING DATE: 1996-06-12
EARLIER APPLICATION NUMBER: 08/694, 078
EARLIER PILING DATE: 1996-08-08
EARLIER APPLICATION NUMBER: 08/781, 802
EARLIER PILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: 08/827, 810
EARLIER PILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 37

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 7
LENGTH: 3147
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: cloned esterase
NAME/KEY: CDS
LOCATION: (245) ..(1231)
US-09-058-260-7

Query Match      11.8%; Score 38.2; DB 3; Length 3147;
Best Local Similarity 47.8%; Pred. No 3.3; Indels 1; Gaps 1;
Matches 141; Conservative 0; Mismatches 153; Indels 1; Gaps 1;

QY    25 GAAGGTGGGCGCCGGGGTGGGCCTTCGCGAACAAGGCCGGGCTCCTCTCTACAGG   84
DB    2386 GGAGGCCCCCTGAGAGGGGGGGGCGCCGCTCTGAGCGCGGGGCGAGAGCGGCTCAAGG   2445
QY    85 GCCCCAGCGCCT -GCCAAGAGAAGTGCTTCGAAGCCCGCGCGAAGAGGGGCAAGGGCT   143
DB    2446 GTGCTGCGCTCTGAGAGGGGAAAGCGCGAGAGAGCCCGGAGGGGCTTCCAGCGCGCG   2505
QY    144 TCCGAGGCGCCCGCGCGCGCAGCAAGAAATTGGCCAGGSCAACGCGCTGAGCGAGCGG   203
DB    2506 CATCTACTCGGGCTTTCCCAAGACGCCCTCCTCTGGGCGCTTGGAGGAGCGG   2565
QY    204 CAGGCGCTTTCTCAGAGAGCGCGGCGAGCGCGCTGTGAGGGGCGCAGAGACCGGATTAAG   263
DB    2566 CGCGCTTCTCCAGAGAGGCGCTTGCGCCCGGCGAGCGGCGGAGCGGCGGCGAGCGCGC   2625
QY    264 AAGCGTCGTGCGCTTGGCCCGGCGAGCGCGCAGATTCCCGCGCGCCCGAGCCCCC   318
DB    2626 CTCCTTAAGGGGCGCTTCTCTCTGCGCCAGGACCGCGCGAGGCGCTTGCGCGC   2680

RESULT 25
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match      11.8%; Score 38.2; DB 3; Length 4403765;
Best Local Similarity 49.8%; Pred. No. 4.1;
Matches 130; Conservative 0; Mismatches 123; Indels 8; Gaps 1;

QY    4 CGTGGGCTCAGACCGCAAGCGAAGGTGCGGGCGCGGCTCGCGGAGCAAGAAGC   63
DB    841343 CGGCGGGGCGCGCGGAGAACCGCGGAGCGCTCGCACTGATGATGCGGGGCGCGGAGC   841402
QY    CGGCGCTGCTCTCTCAGAGGGCGCCAGCGGCGCTGCCAAGAAGAAAGTCTTCGAGCGCCGG   123

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/ ADDRESSER: THOMAS G. PLANT 1501
/ STREET: LILLY CORPORATE CENTER
/ CITY: INDIANAPOLIS
/ STATE: IN
/ COUNTRY: USA
/ ZIP: 46285
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: ASCII(DOS) Text only
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/804,227C
/ FILING DATE: February 21, 1997
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Plant, Thomas, G.
/ REGISTRATION NUMBER: 35,784
/ REFERENCE/DOCKET NUMBER: X-8231
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 317-276-2459
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 43280 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 816..14234
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 14351..19945
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 20010..31199
/ NAME/KEY: CDS
/ LOCATION: 31232..36067
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 36249..41774
/ US-08-804-227C-1

Query Match 11.7%; Score 37.8; DB 2; Length 43280;
Best Local Similarity 45.7%; Pred. No. 4.4;
Matches 132; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 33 GGGCGGGGTGGGCTCGCGGAGCAAGAGCGGGCGCTCTCTAGAGGGCCGAGC 92
DB 18673 GCGCGGGACCGTGCCTGCGGAGCAATGCGGGCGCTCGCGCGAGGCTGCGGT 18614

QY 93 GCGTCCCAAGAGAACTCTGAGAGCCCGGCGAGGAGGGGCGACGGGCTTCCAGGGC 152
DB 18613 GCGCCCAATGATACAGAGAGGTGCGCTGAGTGCAGGCGAGCCGCGCGCGGCGAGCGT 18554

QY 153 CGCGCGCGCGAGCAAGAGTTGGCCAGGGCAAGCGGCTGTAGCGGAGCGGGGAGGCTTT 212
DB 18553 GCGCAGGGGTGAGGGAGGGGCGAGAGGAGTGCCTGCGGAGGTGAGAGCTGCTGCGGCT 18494

QY 213 CTGAGAGAGCGCGGCGAGGCGCGGCTGTGAGAGGGGCGAGAGCCGGGTATAGAAAGCTTGT 272
DB 18493 GCGCCCGACGCGCTGCGAGAGTTGGCCGAGAGCGGGGAGAGTGTGCTGCTGCGAGAGAGCG 18434

QY 273 GCGCTTGGCGCGGCGAGCGCGCAGAGTTCCCGCGCGCGCGCGCGAGCGCCCGCGG 321
DB 18433 GAAGCACCAGGGGTGCTCGAGCTGTGCGCGCGCGCGAGCAAGTCCCGACAGC 18385

RESULT 29
US-08-965-048-5/c
; Sequence 5, Application US/08965048
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/ Patent No. 6323244
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Hong
/ APPLICANT: Freilmer, Nelson
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
/ TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
/ FILE REFERENCE: 7853-093
/ CURRENT APPLICATION NUMBER: US/08/965,048
/ CURRENT FILING DATE: 1997-11-05
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: patentin Ver. 2.0
/ LENGTH: 45716
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-08-965-048-5

Query Match 11.7%; Score 37.8; DB 4; Length 45716;
Best Local Similarity 50.8%; Pred. No. 4.4;
Matches 90; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 117 GCGCGGCGAGGAGAGGGGCGACGGGCTTCCAGGGCTCCCGCGCGCGAGAGAGTTGG 176
DB 5094 GCGCGGAGATCTCTCGCGGACCATGAGCCCTTGCGCCCTGAGCGCGGCGCGCGCGG 5035

QY 177 CGAGGCGACGCGCGCTGAGCGGAGCGGCGAGGGCTTTCTCAAGAGCGCGCGAGCGCGC 236
DB 5034 TCAGGACTGTGTGGGATCCCGAGCGCGCGGCGAGGGCGGAGGCGGAGCGCGGCGAGC 4975

QY 237 GCTGAGGGGCGAGAGCGGGGTATAGAGCTCTGCGCTTGGCCCGGAGCGCGCA 293
DB 4974 GCGCGAGCGGGGCGACCGTCAAGGGCATAGAGGGCGCTCATTTGCGCGCGCGCGCA 4918

RESULT 30
US-08-965-048-6/c
; Sequence 6, Application US/08965048
/ Patent No. 6323244
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Hong
/ APPLICANT: Freilmer, Nelson
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
/ TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
/ FILE REFERENCE: 7853-093
/ CURRENT APPLICATION NUMBER: US/08/965,048
/ CURRENT FILING DATE: 1997-11-05
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO: 6
/ LENGTH: 45989
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-08-965-048-6

Query Match 11.7%; Score 37.8; DB 4; Length 45989;
Best Local Similarity 50.8%; Pred. No. 4.4;
Matches 90; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 117 GCGCGGCGAGGAGAGGGGCGACGGGCTTCCAGGGCTCCCGCGCGCGAGAGAGTTGG 176
DB 5094 GCGCGGAGATCTCTCGCGGACCATGAGCCCTTGCGCCCTGAGCGCGGCGCGCGCGG 5035

QY 177 CGAGGCGACGCGCGCTGAGCGGAGCGGCGAGGGCTTTCTCAAGAGCGCGGCGAGCGCGC 236
DB 5034 TCAGGACTGTGTGGGATCCCGAGCGCGCGGCGAGGGCGGAGGCGGAGCGCGGCGAGC 4975

QY 237 GCTGAGGGGCGAGAGCGGGGTATAGAGCTCTGCGCTTGGCCCGGAGCGCGCA 293
DB 4974 GCGCGAGCGGGGCGACCGTCAAGGGCATAGAGGGCGCTCATTTGCGCGCGCGCGCA 4918

RESULT 31
US-08-483-533-37/c
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Sequence 37, Application US/0848353  
Patent No. 6172047  
GENERAL INFORMATION:  
APPLICANT: Roizman, Bernard  
TITLE OF INVENTION: Method for Treating Tumorigenic  
Diseases  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,533  
FILING DATE: 07-MAR-95  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/419,853  
FILING DATE: 11-APR-95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/861,233  
FILING DATE: 31-MAR-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, James P.  
REGISTRATION NUMBER: 28,491  
REFERENCE/DOCKET NUMBER: 28097/32742  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1292 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-483-533-37

Query Match 11.6%; Score 37.6; DB 3; Length 1292;

Best Local Similarity 46.9%; Pred. No. 4.3;  
Matches 152; Conservative 0; Mismatches 169; Indels 3; Gaps 1;

QY 2 CGCGTGGGTCAGACCGCAAGGAGGTCGGGCGGGGCTTCGCGAGACAAAG 61  
DB 905 CGCCTCGGGGTAACTTACCGAGTTGCGCGGGCGGCTCGCGGCGCAAGCGCGG 846  
QY 62 GCCGGGCTTCGCTCTCTAGAGGCGCCGCGCTGCGCAAGAGAAAGTCTCGAGGCGCG 121  
DB 845 CACGGGCTTCGCGGCGCCAGGCGCGCCGATGACCGCTTCGCGCTCGCGACCGCGCGCG 786  
QY 122 GCGAGGAAAGGAGGCGAGCGGCTTCCAGGCGCGCGCGCGCGAGCAAGAAATTGGCCAG 181  
DB 785 GGAACGAGACCGGTCGGGCGCGCTCGCGGGCCAGAGCGCGGCGCGCGCAAGCGCGG 726  
QY 182 GCAAGCGCGTG---AGCGAGCGGGGCAAGGCTTTCTCAGAGAGCGCGGCGAGCGCGCGC 238  
DB 725 CCGAGGCGCGAGACCAACAGATGGCGCACCGGAGCGAGGCGCAACCGCGCGCGC 666  
QY 239 TCGAGGCGCGAGAGACCGGGTATTAAGAGCTGCTGCGCTTGCCTCGGCGAGCGCGAGTTTC 298  
DB 665 GGGTGGCGGGGTCGGGCGGGGTCGCGGGGTCGCGGGGTCGCGGGGTCGCGGGGTCGCG 606  
QY 299 CCGGCGCGCGCGCGAGCGCGCGCGC 322

DB 605 CCGGCGCGCGCTTCGCGCGCGCGCGC 582

RESULT 32

US-09-283-471A-37/c

Sequence 37, Application US/09283471A

Patent No. 6340673

GENERAL INFORMATION:

APPLICANT: Roizman, Bernard

TITLE OF INVENTION: Method For Treating Tumorigenic Diseases

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/283,471A

FILING DATE: 04-APR-1999

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/861,233

FILING DATE: 31-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/419,853

FILING DATE: 11-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/483,533

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, James P.

REGISTRATION NUMBER: 28,491

REFERENCE/DOCKET NUMBER: 27373/32742A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 1292 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-283-471A-37

Query Match 11.6%; Score 37.6; DB 4; Length 1292;

Best Local Similarity 46.9%; Pred. No. 4.3;  
Matches 152; Conservative 0; Mismatches 169; Indels 3; Gaps 1;

QY 2 CGCGTGGGTCAGACCGCAAGGAGGTCGGGCGGGGCTTCGCGAGACAAAG 61  
DB 905 CGCCTCGGGGTAACTTACCGAGTTGCGCGGGCGGCTCGCGGCGCAAGCGCGG 846  
QY 62 GCCGGGCTTCGCTCTCTAGAGGCGCCGCGCTGCGCAAGAGAAAGTCTCGAGGCGCG 121  
DB 845 CACGGGCTTCGCGGCGCCAGGCGCGCCGATGACCGCTTCGCGCTCGCGACCGCGCGC 786  
QY 122 GCGAGGAAAGGAGGCGAGCGGCTTCCAGGCGCGCGCGCGCGAGCAAGAAATTGGCCAG 181  
DB 785 GGAACGAGACCGGTCGGGCGCGCTCGCGGGCCAGAGCGCGGCGCGCGCAAGCGCGG 726  
QY 182 GCAAGCGCGTG---AGCGAGCGGGGCAAGGCTTTCTCAGAGAGCGCGGCGAGCGCGCGC 238  
DB 725 CCGAGGCGCGAGACCAACAGATGGCGCACCGGAGCGAGGCGCAACCGCGCGCGC 666

Qy	239	TTGAGGGGGCGAGGACCGGGGTATATAGAAAGCTCTGTGAGCTTGTGCGGAGCGGACGAGTTC	298
Db	665	GGGTCCGGGGGTCTGCGGGGGGTGCGGGGGGTGCGGGGAGTCCGCGGGGACT	606
Qy	299	CCGCGCGGCGCCCGAGCGCCCGCGCG	322
Db	605	CCGAGCGCCCTCTCCCGCGCGCGCC	582

RESULT 33

US-08-943-731-5/c  
Sequence 5, Application US/08943731  
Patent No. 6265157  
GENERAL INFORMATION:  
APPLICANT: PROCKOP, DARWIN J.  
APPLICANT: SPOTILIA, LORETTA D.  
APPLICANT: DELTAS, CONSTANTINOS D.  
APPLICANT: SEREDA, IARISA  
APPLICANT: LARSON, ANDREA W.  
APPLICANT: PACR, MICHAEL  
APPLICANT: COLIGE, ALAIN  
APPLICANT: EARLY, JAMES  
APPLICANT: KOROKO, JARMO  
APPLICANT: ALA-KOKKO, IRENA, et al.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING  
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES  
NUMBER OF SEQUENCES: 666  
CORRESPONDENCE ADDRESS  
ADDRESSEE: PAUTICH, SCHWARZE JACOBS & NADEL, P.C.  
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND  
STREET: FLA.  
CITY: PHILADELPHIA  
STATE: PA

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentm Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,731  
FILING DATE: 03-OCT-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/212,322  
FILING DATE: 14-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/803,628  
FILING DATE: 03-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: DOYLE LEARY Ph.D., KATHRYN  
REGISTRATION NUMBER: 36,317  
REFERENCE/DOCKET NUMBER: 9598-27  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-965-1284  
TELEFAX: 215-567-2991  
TELEX: 831-494  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20084 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-943-731-5

Query Match	11.6%	Score 37.6;	DB 3;	Length 2084;
Best Local Similarity	53.4%;			
Matches 79;	Conservative	0;	Mismatches	0; Gaps
 176 GCCAGGCGACGGCCGTAGCGGAGCGGGCGGCCTTTCATGAGAGGCCGAGGCCCG 235				

Db	QY	Dp	QY	Db	QY	Db
3209	GCAGCGCCCGCGCCCGCCGACATGCGCTGAGCGGAGTCTAGCTGCGCGCGCTCGGGGCGGGCGG	3150				
236	CGCTGAGAGGGCGCAGAGACCGAGTATTAAGAAACCTCTGTGGCCCTTTCGCCGGGCGAGCTCCGAGG	295				
3149	CGCCCGGACCGCGCGCGCGCGCGAGGTGGAGCGGCCCTTTCCTTCCCTTTCGCCGCCCGC	3090				
296	TTCCCGCGCGCGCCCGAGCCCCCGCGGCT	323				
3089	CTGCACAAAGCCCCCATTTACGCGCGGGCC	3062				

RESULT 34

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US-08-458-568A-3
Sequence 3, Application US/08458568A
Patent No. 5821339
GENERAL INFORMATION:
APPLICANT: Schaffer, Priscilla A.
APPLICANT: Yeh, Lily
TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus
TITLE OF INVENTION: Infections
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn, Kurtz, Mackiewicz & No. 5821339.ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA

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1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Floppy disk
3 COMPUTER: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: WordPerfect 5.1
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/08/458,568A
8 FILING DATE: 02-JUNE-1995
9 CLASSIFICATION: 435
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US 08/065,146
12 FILING DATE: 05-MAY-1993
13 CLASSIFICATION: 435
14 ATTORNEY/AGENT INFORMATION:
15 NAME: leary Ph.D., Kathryn R.
16 REGISTRATION NUMBER: 36,317
17 REFERENCE/DOCKET NUMBER: DCSI-0029
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: (215) 568-3100
20 TELEFAX: (215) 568-4439
21 INFORMATION FOR SEQ ID NO: 3:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 702 base pairs
24 TYPE: nucleic acid
25 STRANDEDNESS: double
26 TOPOLOGY: linear
27 MOLECULE TYPE: DNA (genomic)
28 HYPOTHEITICAL: NO
29 ANTI-SENSE: NO
30 ORIGINAL SOURCE:
31 ORGANISM: Herpes simplex virus
32 STRAIN: Herpes Simplex Virus Type 1
33 FEATURE:
34 NAME/KEY: CDS
35 LOCATION: 1..702
36 US-08-458-568A-3

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Query Match	11.6%	Score 37.4	DB 1	Length 702
Best Local Similarity	47.8%	Pred. No. 4.7		
Matches 133; Conservative	0;	Mismatches 151;	Indels 1;	Gaps 1
OY	2	CGGTCGGCTCACAACGCAGAAAGTGAAGCCCGGGATGAGCCTCCGCGAGAACAAG	61	
Db	145	CGCGCGGGGTCTCGGGGCTCGGGGCTCGCGGGGTGCGCGGGATCCGCGGGGCTCC	204	

QY 62 GCCGGGCTGCTCTCTCAGAGGGCCCGAGGCTGCGAAGAAAGTCTCGAGGCCG 121  
DB 205 GGGGCCCCCTCCCGCCCGGCGCTCGAGGCGCGAGCGCGCGGTCCTCGCGTGAGC 264  
QY 122 GCGAGGAAAGGGGCGACGGGCTTCCAGAGCCCGCGCGCGAGAGAAATTGGCCAG 181  
DB 265 CGCAGCGGAGGGCGAGGCGCGCGAGAAAGGGCGCGAGGGGGGTGGAGGGG 324  
QY 182 GCAAGGCGCTGAGCGGAGCGGAGGCTTCTCAGAGCGCGCGGAGGCG-CGGCGCTG 240  
DB 325 TCAAGCCCCCGCCCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 384  
QY 241 GAGGGCGGAGGAGCGGCTATTAAGAGCTCTGCGCTTGGCCGCGAGCGG 291  
DB 385 GTGGGCGGCGCTCTGCGCGCGAGCTGGGCGGGGGGCTGTCCGCGAGTGC 435

RESULT 35  
US-09-962-665-5  
; Sequence 5, Application US/09962665  
; Patent No. 6537759  
; GENERAL INFORMATION:  
; APPLICANT: Stanton, Jr., Vincent P.  
; TITLE OF INVENTION: POLY(POLYGLUTAMATE SYNTHETASE GENE SEQUENCE  
; TITLE OF INVENTION: VARIANCES HAVING UTILITY IN DETERMINING THE  
; TITLE OF INVENTION: TREATMENT OF DISEASE  
; FILE REFERENCE: 11926-015004  
; CURRENT APPLICATION NUMBER: US/09/962,665  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/558,659  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 09/596,033  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 09/357,743  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 09/357,024  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: 60/093,484  
; PRIOR FILING DATE: 1998-07-20  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 3772  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 431, 441  
; OTHER INFORMATION: n = a or g  
; NAME/KEY: misc\_feature  
; LOCATION: 498  
; OTHER INFORMATION: n = c or t  
; NAME/KEY: misc\_feature  
; LOCATION: 579, 599  
; OTHER INFORMATION: n = g or c  
US-09-962-665-5

Query Match 11.6%; Score 37.4; DB 4; Length 3772;  
Best Local Similarity 54.8%; Pred. No. 4.9;  
Matches 74; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 114 GAGGCGCGGCGAGGAGGAGGCGGCTTCCAGAGGCCCGCGCGCGAGAGAAAT 173  
DB 1020 GGGCGCGAGGGGCGGCTCGAGGCGCGCGCGCGCGCGAGGAGGAGGAGG 1079  
QY 174 TGGCCAGGAGGCGGCGGCTTCTCAGAGCGCGCGCGCGCGAGGCG 233  
DB 1080 GCGCGCTGACCGCGCGGTGAGCGGCTGGAGAGGCGCGCGCGCGCGCG 1139  
QY 234 GCGCGCTGAGGCGG 248  
DB 1140 GTGGGTGGAGGAGGTG 1154

RESULT 36  
US-08-458-568A-11  
; Sequence 11, Application US/08458568A  
; Patent No. 5821339  
; GENERAL INFORMATION:  
; APPLICANT: Schaffer, Priscilla A.  
; APPLICANT: Yeh, Lily  
; TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus  
; TITLE OF INVENTION: Infections  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris  
; STREET: One Liberty Place, 46th floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,568A  
; FILING DATE: 02-JUNE-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/065,146  
; FILING DATE: 05-MAY-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Leary Ph.D., Kathryn R.  
; REGISTRATION NUMBER: 36,317  
; REFERENCE/DOCKET NUMBER: DPCI-0029  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12001 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Herpes simplex virus  
; STRAIN: Herpes Simplex Virus Type 1  
US-08-458-568A-11

Query Match 11.6%; Score 37.4; DB 1; Length 12001;  
Best Local Similarity 47.8%; Pred. No. 5.1;  
Matches 139; Conservative 0; Mismatches 151; Indels 1; Gaps 1;

QY 2 GCGGTGGGTCAAGCCGAAAGCGAGGTGCGGCGCGGCGCTTCCGAGCAAG 61  
DB 514 CGCGGGGGGTGCGCGGGGTGCGCGGGGTGCGCGGGGTGCGCGGGGTGCG 573  
QY 62 GCGGCGCTGCTCTCTCAGAGGGCGCGCGCGCTGCGAAGAAAGTCTGAGGCCG 121  
DB 574 GCGGCGCTTCCCGCGCGCGCGGTGCGAGGCGCGCGCGCGCGAGTCTCCGCTGACG 633  
QY 122 GCGAGGAAAGGGGCGACGGGCTTCCAGAGGCCCGCGCGCGAGAGAAATTGGCCAG 181  
DB 634 CGCAGCGGAGGCGAGGCGCGCGGAGAGGCGGAGGCGCGCGCGCGCGGAGGAGG 693  
QY 182 GCAAGGCGCTGAGCGGAGCGGAGGCTTCTCAGAGCGCGCGGAGGCG-CGGCGCTG 240  
DB 694 TCAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGGTGCGGCGCGCGCGCGCGCG 753

QY 241 GAGGCGAGAGACCGGGTATAGAACCTGTGCGCTTCCCGGAGCCG 291  
DB 754 GTGGCGCGGGCTCTGGCGCGCACTCGGGCGGGGGCTGTCCGGCAGTGC 804

RESULT 37  
US-09-252-991A-13576  
; Sequence 13576, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 13576  
; LENGTH: 732  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13576

Query Match 11.5%; Score 37.2; DB 4; Length 732;  
Best Local Similarity 48.6%; Pred. No. 5.2; Mismatches 108; Indels 0; Gaps 0;  
Matches 102; Conservative 0;

QY 107 AGTCTCGAGGCGCGGCGAGGAGGCGGCTTCCAGGCGCGCGCGCAGC 166  
DB 480 ACTTCCTGCTGCGCGCGCGCGCGAGCGGCTTCCGCGCGCGCGCGCGCAGC 539  
QY 167 AGGAAGTTGGCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 226  
DB 540 TCGAGAGGCG 599  
QY 227 CGAGGCG 286  
DB 600 CTTTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 659  
QY 287 AGCGCGAGGTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 316  
DB 660 TGGCGAGGCTCAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 689

RESULT 38  
US-09-252-991A-13471  
; Sequence 13471, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 13471  
; LENGTH: 891  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13471

Query Match 11.5%; Score 37.2; DB 4; Length 891;  
Best Local Similarity 48.6%; Pred. No. 5.2; Mismatches 108; Indels 0; Gaps 0;  
Matches 102; Conservative 0;

QY 107 AGTCTCGAGGCGCGGCGAGGAGGAGGCGGCTTCCAGGCGCGCGCGCAGC 166  
DB 22 ACTTCCTGCTGCGCGCGCGCGCGCGAGCGGTTCCGCGCGCGCGCGCGCGCGCAGC 81  
QY 167 AGGAAGTTGGCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 226  
DB 82 TCGAGAGGCG 141  
QY 227 CGAGGCG 286  
DB 142 CTTTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 201  
QY 287 AGCGCGAGGTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 316  
DB 202 TGGCGAGGCTCAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 231

RESULT 39  
US-09-252-991A-13766/c  
; Sequence 13766, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 13766  
; LENGTH: 1098  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13766

Query Match 11.5%; Score 37.2; DB 4; Length 1098;  
Best Local Similarity 48.6%; Pred. No. 5.2; Mismatches 108; Indels 0; Gaps 0;  
Matches 102; Conservative 0;

QY 107 AGTCTCGAGGCGCGGCGAGGAGGAGGCGGCTTCCAGGCGCGCGCGCAGC 166  
DB 797 ACTTCCTGCTGCGCGCGCGCGCGCGAGCGGTTCCGCGCGCGCGCGCGCGCAGC 738  
QY 167 AGGAAGTTGGCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 226  
DB 737 TCGAGAGGCG 678  
QY 227 CGAGGCG 286  
DB 677 CTTTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 618  
QY 287 AGCGCGAGGTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 316  
DB 617 TGGCGAGGCTCAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 588

RESULT 40  
US-08-278-729A-32/c  
; Sequence 32, Application US/08278729A  
; Patent No. 5650276  
; GENERAL INFORMATION:  
; APPLICANT: SMART, JOHN  
; APPLICANT: OPPERMAN, HERMAN  
; APPLICANT: OZKAYNAK, ENGİN  
; APPLICANT: KUBERASAMPATH, THANGAVEL  
; APPLICANT: RUEGER, DAVID C.  
; APPLICANT: PANG, ROY H. L.  
; APPLICANT: COHEN, CHARLES M.

TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES  
STREET: 45 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 01748  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/278,729A  
FILING DATE: 20-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: PITCHER Esq., EDMUND R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-058CPFW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508) 435-9001  
TELEFAX: (508) 435-6951  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1247 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 84..1199  
OTHER INFORMATION: /product= "GDP-1"  
US-08-278-729A-32

Query Match 11.5%; Score 37.2; DB 1; Length 1247;

Best Local Similarity 48.6%; Pred. No. 5.2; Mismatches 108; Indels 0; Gaps 0;

Matches 102; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 113 CGAGGCCCGGCGAGGAGGGGCGACGGGCTTCCAGAGGCCCGCGCGCAGCAGGAAG 172  
DB 838 CGCGGCCGGGCGAGGGGTGCGACAGCGCGGGTCAACAGCAGCAGCGAGGCC 779  
QY 173 TTGGCTCAGGCGACGCGCTGAGCGGAGCGGGCAGGGCTTTCTCAGAGCGCGGGCGAGGC 232  
DB 778 TCGGCCAGGCGCGCGAGGCGCGGAGGGGCCCGGGGGCGTAGCGCCAGCGCCAGGCGGAGG 719  
QY 233 CGAGCGCTGAGGGGCGAGGACCGGGGTATAGAAAGCTTCGTGGCCCTTGCCCGGGCAGCGGC 292  
DB 718 CTGCGCGGCGCATGAGGCGTTGCGAGGCCCAAGCGGCGCCCAAGCAGCTCCGCGCGCACTGSC 659  
QY 293 AGTTTCCCCCGCGCGCGCCGAGCGCCCGCGGC 322  
DB 658 GCGCCCGAGGGCGGGCACCAACTGCGCGAGC 629

Search completed: November 6, 2003, 09:05:47  
Job time : 63.0256 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: November 6, 2003, 08:07:17 ; Search time 242.663 Seconds  
(Without alignments)  
4247.375 Million cell updates/sec

Title: US-10-081-817a-19\_COPY\_229\_551

Perfect score: 323

Sequence: 1 GCGCGTGGGTGAGACGCA.....GCGCCCCGAGCCCCGCGCC 323

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 214154 seqs, 159547879 residues

Total number of hits satisfying chosen parameters: 4282708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications\_NA:\*

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- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
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- 12: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	323	100.0	547	13	US-10-081-817-19
2	316.4	98.0	1794	12	US-10-059-579-120
3	116	35.9	561	14	US-10-237-435-6
4	78	24.1	569	12	US-10-210-951-27
5	78	24.1	569	12	US-10-211-884-27
6	78	24.1	570	9	US-09-989-722-407
7	78	24.1	570	9	US-09-989-723-407
8	78	24.1	570	9	US-09-989-727-407
9	78	24.1	570	9	US-09-989-731-407
10	78	24.1	570	10	US-09-989-732-407
11	78	24.1	570	10	US-09-989-732-407
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27	78	24.1	570	10	US-09-989-721-407	Sequence 407, App
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38	78	24.1	570	10	US-09-989-721-407	Sequence 407, App
39	78	24.1	570	10	US-09-989-721-407	Sequence 407, App
40	78	24.1	570	10	US-09-989-721-407	Sequence 407, App
41	78	24.1	570	10	US-09-989-721-407	Sequence 407, App
42	78	24.1	570	10	US-09-989-721-407	Sequence 407, App
43	78	24.1	570	10	US-09-989-721-407	Sequence 407, App
44	78	24.1	570	10	US-09-989-721-407	Sequence 407, App
45	78	24.1	570	10	US-09-989-721-407	Sequence 407, App

#### ALIGNMENTS

RESULT 1

US-10-081-817-19

Sequence 19, Application US/10081817

Publication No. US20020183501A1

GENERAL INFORMATION:

APPLICANT: Polyak, Kornelia

APPLICANT: Portier, Dale

APPLICANT: Sgroi, Dennis

TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE

FILE REFERENCE: 00530-094001

CURRENT APPLICATION NUMBER: US/10/081,817

PRIOR FILING DATE: 2002-05-31

PRIOR APPLICATION NUMBER: 60/270,973

PRIOR FILING DATE: 2002-01-25

PRIOR APPLICATION NUMBER: 60/351,908

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 19

LENGTH: 547

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 186

OTHER INFORMATION: n = C or G

US-10-081-817-19

Query Match 100.0%; Score 323; DB 13; Length 547;

Best Local Similarity 100.0%; Pred. No. 6.2e-67;

Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GCGCGGCGGTGAGACCGAAGCGAAGGTGCGGCGGCGGTGCGGCGGCGAAGCAAA	60
Db	225	GCGCGGCGGTGAGACCGAAGCGAAGGTGCGGCGGCGGTGCGGCGGCGAAGCAAA	284
Qy	61	GCGCGGCGGTGAGACCGAAGCGAAGGTGCGGCGGCGGTGCGGCGGCGAAGCAAA	120

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Db      285 GGGCGGGGCTGCTCTCTCAGAGAGGGCCGACGGCCTGCGCAAGAGAAATCTCGAGGGCCC 344
Qy      121 GGGCGAGGAGGGGGGCGAGGGCTTCCAGAGGCCCGCGCGCCGACAGAGAAATGGCCGAG 180
Db      345 GGGCGAGGAGGGGGGCGAGGGCTTCCAGAGGCCCGCGCGCCGACAGAGAAATGGCCGAG 404
Qy      181 GGCACGGCCGCTGAGCGAGCGGGCGAGGGCTTTCTCAGAGACGCGGGCGAGGGCGGCTG 240
Db      405 GGCACGGCCGCTGAGCGAGCGGGCGAGGGCTTTCTCAGAGACGCGGGCGAGGGCGGCTG 464
Qy      241 GAGGGGCGAGGACCGGGGTATTAAGAGCTCTGCGCTTCCGCGGAGCGGAGAGTTCC 300
Db      465 GAGGGGCGAGGACCGGGGTATTAAGAGCTCTGCGCTTCCGCGGAGCGGAGAGTTCC 524
Qy      301 GCGCGCGCCCGGAGCGCCCGCGCC 323
Db      525 GCGCGCGCCCGGAGCGCCCGCGCC 547

RESULT 2
; US-10-059-579-120
; Sequence 120, Application US/10059579
; Publication No. US20030138783A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: SUKUMAR, Sarabwati
; APPLICANT: EVRON, Elia
; APPLICANT: DOOLEY, William C.
; APPLICANT: DAVIDSON, Nancy Jo.
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
; FILE REFERENCE: JHU1630-1
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US 09/771,357
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 120
; LENGTH: 1794
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (359)..(359)
; OTHER INFORMATION: n is any nucleotide
US-10-059-579-120

Query Match      98.0%; Score 316.4; DB 12; Length 1794;
Best Local Similarity 99.7%; Pred. No. 1.6e-65;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 TGGGCTCAGACCGCAAGAGGTCGGGCGCGGCTGCGCTCCCGAGACAAAGGCGG 65
Db      854 TGGGCTCAGACCGCAAGAGGTCGGGCGCGGCTGCGCTCCCGAGACAAAGGCGG 913
Qy      66 GGCCTGCTCTCTCAGAGGGCCCGACGCTGCGCAAGAGAAATCTCGAGGGCCGAGCA 125
Db      914 GGCCTGCTCTCTCAGAGGGCCCGACGCTGCGCAAGAGAAATCTCGAGGGCCGAGCA 973
Qy      126 GGGAGGGGGGACCGGGCTTCCAGAGGCCCGCGCGCGAGAGAAATTTGGCGAGGCGAC 185
Db      974 GGGAGGGGGGACCGGGCTTCCAGAGGCCCGCGCGCGAGAGAAATTTGGCGAGGCGAC 1033
Qy      186 GGCCTGAGCGGAGCGGGCGAGGGCTTTCTCAGAGACGCGGGCGAGGGCGGCTGAGAGG 245
Db      1034 GGCCTGAGCGGAGCGGGCGAGGGCTTTCTCAGAGACGCGGGCGAGGGCGGCTGAGAGG 1093
Qy      246 GCGAGAGCCGGGTATTAAGAGCTCTGCGCTTCCGCGGAGCGCGAGAGTTCCCGCGCC 305
Db      1094 GCGAGAGCCGGGTATTAAGAGCTCTGCGCTTCCGCGGAGCGCGAGAGTTCCCGCGCC 1153
Qy      306 GCGCGGAGCGCCCGCGCC 323
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Db      1154 GCGCGGAGCGCCCGCGCC 1171

RESULT 3
; US-10-237-435-6
; Sequence 6, Application US/10237435
; Publication No. US20030124580A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Spiro, Peter A.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: LONG SURFACTANT MOLECULES
; FILE REFERENCE: PB-0019 US
; CURRENT APPLICATION NUMBER: US/10/237,435
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/317,822
; PRIOR FILING DATE: 09-07-2001
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO: 6
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124580A1 242745.1
US-10-237-435-6

Query Match      35.9%; Score 116; DB 14; Length 561;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      208 GCTTCTCAGAGCGCGGCGGAGGCTGCGAGGGCGAGACCGGGTATTAAGAGC 267
Db      1 GCTTCTCAGAGCGCGGCGGAGGCTGCGAGGGCGAGACCGGGTATTAAGAGC 60
Qy      268 CTCGTGAGCTTGGCGGCGAGCGCGAGGTTCCCGCGGCGCCCGAGCCCGCGCC 323
Db      61 CTCGTGAGCTTGGCGGCGAGCGCGAGGTTCCCGCGGCGCCCGAGCCCGCGCC 116

RESULT 4
; US-10-210-951-27
; Sequence 27, Application US/10210951
; Publication No. US20030170228A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2931R1C1
; CURRENT APPLICATION NUMBER: US/10/210,951
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
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;; PRIOR FILING DATE: 1997-10-10
;; PRIOR APPLICATION NUMBER: 60/063755
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063045
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063046
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/06511
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/066772
;; PRIOR FILING DATE: 1997-11-24
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 258
;; SEQ ID NO 27
;; LENGTH: 569
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-210-951-27
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Query Match          24.1%; Score 78; DB 12; Length 569;
Best Local Similarity 100.0%; Pred. No. 1,1e-09;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      246 GCGAGGACCGGGATATAGAGCCTTGCGCCGCGGCGAGCGAGTTCCCGCGCC 305
DB      1 GCGAGGACCGGGATATAGAGCCTTGCGCCGCGGCGAGCGAGTTCCCGCGCC 60
QY      306 GCGCCGAGCGCCCGCGCGCC 323
DB      61 GCGCCGAGCGCCCGCGCGCC 78
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RESULT 5
US-10-211-884-27
; Sequence 27, Application US/10211884
; Publication No. US20030175900A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guirney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Masters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Picti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2931R1C1
; CURRENT APPLICATION NUMBER: US/10/211,884
; PRIOR APPLICATION NUMBER: 2002-08-02
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
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; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
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;; PRIOR FILING DATE: 1997-11-24
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 258
;; SEQ ID NO 27
;; LENGTH: 569
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-211-884-27
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Query Match          24.1%; Score 78; DB 12; Length 569;
Best Local Similarity 100.0%; Pred. No. 1,1e-09;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      246 GCGAGGACCGGGATATAGAGCCTTGCGCCGCGGCGAGCGAGTTCCCGCGCC 305
DB      1 GCGAGGACCGGGATATAGAGCCTTGCGCCGCGGCGAGCGAGTTCCCGCGCC 60
QY      306 GCGCCGAGCGCCCGCGCGCC 323
DB      61 GCGCCGAGCGCCCGCGCGCC 78
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RESULT 6
US-09-989-722-407
; Sequence 407, Application US/09989722
; Patent No. US2002072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guirney, Austin L.
; APPLICANT: Kjaavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; PRIOR APPLICATION NUMBER: 2001-11-19
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
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Fri Nov 7 08:10:02 2003

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2 PRIOR APPLICATION NUMBER: 60/087106  
3 PRIOR FILING DATE: 1998-05-28  
4 PRIOR APPLICATION NUMBER: 60/087607  
5 PRIOR FILING DATE: 1998-06-02  
6 PRIOR APPLICATION NUMBER: 60/087609  
7 PRIOR FILING DATE: 1998-06-02  
8 PRIOR APPLICATION NUMBER: 60/087759  
9 PRIOR FILING DATE: 1998-06-02  
10 PRIOR APPLICATION NUMBER: 60/087827  
11 PRIOR FILING DATE: 1998-06-03  
12 PRIOR APPLICATION NUMBER: 60/088021  
13 PRIOR FILING DATE: 1998-06-04  
14 PRIOR APPLICATION NUMBER: 60/088025  
15 PRIOR FILING DATE: 1998-06-04  
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23 PRIOR FILING DATE: 1998-06-04  
24 PRIOR APPLICATION NUMBER: 60/088033  
25 PRIOR FILING DATE: 1998-06-04  
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31 PRIOR FILING DATE: 1998-06-05  
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33 PRIOR FILING DATE: 1998-06-05  
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35 PRIOR FILING DATE: 1998-06-05  
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59 PRIOR FILING DATE: 1998-06-16  
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72 PRIOR APPLICATION NUMBER: 60/089600  
73 PRIOR FILING DATE: 1998-06-17

1 PRIOR APPLICATION NUMBER: 60/089653  
2 PRIOR FILING DATE: 1998-06-17  
3 PRIOR APPLICATION NUMBER: 60/089801  
4 PRIOR FILING DATE: 1998-06-18  
5 PRIOR APPLICATION NUMBER: 60/089907  
6 PRIOR FILING DATE: 1998-06-18  
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8 PRIOR FILING DATE: 1998-06-18  
9 PRIOR APPLICATION NUMBER: 60/089947  
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25 PRIOR APPLICATION NUMBER: 60/090429  
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27 PRIOR APPLICATION NUMBER: 60/090431  
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36 PRIOR FILING DATE: 1998-06-24  
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44 PRIOR FILING DATE: 1998-06-24  
45 PRIOR APPLICATION NUMBER: 60/090676  
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57 PRIOR APPLICATION NUMBER: 60/090862  
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60 PRIOR FILING DATE: 1998-06-26  
61 PRIOR APPLICATION NUMBER: 60/091360  
62 PRIOR FILING DATE: 1998-07-01  
63 PRIOR APPLICATION NUMBER: 60/091478  
64 PRIOR FILING DATE: 1998-07-02  
65 PRIOR APPLICATION NUMBER: 60/091544  
66 PRIOR FILING DATE: 1998-07-02  
67 PRIOR APPLICATION NUMBER: 60/091519  
68 PRIOR FILING DATE: 1998-07-02  
69 PRIOR APPLICATION NUMBER: 60/091626  
70 PRIOR FILING DATE: 1998-07-02  
71 PRIOR APPLICATION NUMBER: 60/091633  
72 PRIOR FILING DATE: 1998-07-02  
73 PRIOR APPLICATION NUMBER: 60/091978

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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 9; Length 570;
Best Local Similarity 100.0%; Pred. No. 1,1e-09;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 246 GCGAGACCGGGGTAAAGACCTTCGTGGCTCCCGGCGAGCGAGTTCCCGCGC 305
Db 1 GCGAGACCGGGGTAAAGACCTTCGTGGCTCCCGGCGAGCGAGTTCCCGCGC 60

Oy 306 GCGCGAGCGCGCGCGCGC 323
Db 61 GCGCGAGCGCGCGCGC 78

RESULT 7
US-09-989-723-407
Sequence 407, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Inc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C62
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US/09/989,723
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28

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Patent No. US20020072496A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: F2730P1C56
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; APPLICANT: Tuma, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; Patent No. US20020103125A1
; GENERAL INFORMATION:
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; APPLICANT: Borstein, David
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C70
; CURRENT FILING DATE: 2001-11-20
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PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred.No. 1.1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 306 GCGCGAGCGCCCGCGCC 323  
Db 61 GCGCGAGCGCCCGCGCC 78

RESULT 11  
US-09-989-732-407  
Sequence 407, Application US/09989732  
Patent No. US20020123463A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bockstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eacou, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Gurney, Austen L.  
APPLICANT: Gurney, Austen L.  
APPLICANT: Kijavik, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C57  
CURRENT FILING DATE: 2001-11-19  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 10; Length 570;  
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DB 1 GCGAGAGCGGGATATAGAGCCTGTGGCTTGGCGGCGCGCGAGTTCCCGCGCC 60  
QY 306 GCGCGAGCGCCCGCGCC 323

Db 61 GCGCGAGCGCCCGCGCC 78  
RESULT 12  
US-09-991-073-407  
Sequence 407: Application US/09991073  
Patent No. US2002012756A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Grimsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
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APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C5  
CURRENT APPLICATION NUMBER: US/09/991, 073  
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PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 GCGAGGACCGGATATAGAGCTCGTGGCTTGGCCGGGACAGCCGAGATTCCCGGCGC 305  
Db 1 GCGAGGACCGGATATAGAGCTCGTGGCTTGGCCGGGACAGCCGAGATTCCCGGCGC 60  
Qy 306 GCGCGGAGCGCCGCGCGCGC 323  
Db 61 GCGCGGAGCGCCGCGCGCGC 78

RESULT 13  
US-09-990-442-407  
Sequence 407, Application US/09990442  
Patent No. US2002013252A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Ealon, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
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APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
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APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C  
CURRENT APPLICATION NUMBER: US/09/990,442  
PRIOR FILING DATE: 2001-11-14  
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Query Match      24.1%; Score 78; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
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QY      306 GCCCGGAGCCCGCCGCGCC 323
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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APPLICANT: Gerber, Hanspeter
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; Patent No. US20020137075A1  
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Zhang, Zemin
; APPLICANT: Wood, William I.
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; APPLICANT: Fong, Sherman
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Eaton, Dan L.
; APPLICANT: Desnoyers, Luc

TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C22
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 APPLICANT: Botstein, David  
 APPLICANT: Desnovers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrata, Napoleone

Fri Nov 7 08:10:02 2003

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APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijaviri, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
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/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Deenoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.

/ APPLICANT: Goddard, Audrey
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/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
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APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnuyers, Luc  
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;; PRIOR FILING DATE: 1998-06-26  
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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 10; Length 570;  
Best local similarity 100.0%; Pred. No. 1,1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 GCGAGGACCGCGGTATAGAGCTCGTGGCTTCCCGGACGCGCCAGATTCCCGCGCC 305  
Db 1 GCGAGGACCGCGGTATAGAGCTCGTGGCTTCCCGGACGCGCCAGATTCCCGCGCC 60  
Qy 306 GCGCGGAGCGCGCGCGCC 323  
Db 61 GCGCGGAGCGCGCGCGCC 78

## RESULT 21

US-09-980-444-407  
;; Sequence 407; Application US/09990444  
;; Publication No. US20020193300A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Bocstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Baton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary B.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730P1C19  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1997-11-24  
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PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 GCGGAGACCGGCTATAGAAGCCTCTGCGCTTGCCTCCGCGACCCGAGGTTCCCGCGCC 305  
Db 1 GCGGAGACCGGCTATAGAAGCCTCTGCGCTTGCCTCCGCGACCCGAGGTTCCCGCGCC 60  
Qy 306 GCGCGAGACCCCGCGCGCC 323  
Db 61 GCGCGAGACCCCGCGCGCC 78

## RESULT 22

US-09-991-181-407

Sequence 407, Application US/09991181

Publication No. US2002019761SA1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Bolstein, David

APPLICANT: Deenoyers, Luc

APPLICANT: Ealon, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gettisen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P27301C53  
CURRENT FILING DATE: 2001-11-16  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/049787  
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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-06-25  
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;; PRIOR FILING DATE: 1998-06-25

;; PRIOR APPLICATION NUMBER: 60/090690  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090694  
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;; PRIOR FILING DATE: 1998-06-26  
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;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1, 1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 GCGAGACCGGGTATPAAGCTTCGTGCGCCGCGAGCCGAGTTCCCGCGC 305  
Db 1 GCGAGACCGGGTATPAAGCTTCGTGCGCCGCGAGCCGAGTTCCCGCGC 60  
Qy 306 GCGCCGAGCCCGCGCC 323  
Db 61 GCGCCGAGCCCGCGCC 78

RESULT 23  
US-09-988-730-407  
; Sequence 407, Application US/09989730  
; Publication No. US20020197674A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
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; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC69  
CURRENT APPLICATION NUMBER: us/09/989,730  
CURRENT FILING DATE: 2001-11-20  
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PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match      24.1%; Score 78; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 1,1e-09;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      246 GCGAGAGACGGGGATAGAAAGCTCGTGGCTTGGCCGGGACCCAGGTTCCCGCCG 305
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DB      1 GCGAGAGACGGGGATAGAAAGCTCGTGGCTTGGCCGGGACCCAGGTTCCCGCCG 60
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QY      306 GCCCGAGCCCGCCGCC 323
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DB      61 GCCCGAGCCCGCCGCC 78
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RESULT 24
US-09-990-436-407
; Sequence 407, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guirney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C14

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; PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1,1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 GCGAGGACCGGTTAAGAGCTTGGTCCCGGAGCGGAGTTCCCGGCC 305  
Db 1 GCGAGGACCGGTTAAGAGCTTGGTCCCGGAGCGGAGTTCCCGGCC 60  
Qy 306 GCGCGGAGCGCCCGCGCC 323  
Db 61 GCGCGGAGCGCCCGCGCC 78

RESULT 25  
US-09-993-687-407  
Sequence 407, Application US/09993687  
Publication No. US20020198149A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary B.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gueney, Austin L.  
APPLICANT: Kijavini, Ivay A.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C11  
CURRENT APPLICATION NUMBER: US/09/993,687  
CURRENT FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/049787

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; PRIOR FILING DATE: 1998-07-09

Query Match          24.1%  Score 78;  DB 10;  Length 570;
Best Local Similarity 100.0%;  Pred. No. 11e-09;
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Qy      306  GCGCCGAGCGCCCGCGCGCC 323
Db      61  GCGCCGAGCGCCCGCGCGCC 78

RESULT 26
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; Sequence 407, Application US/09989734
; Publication No. US20030003531A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnuyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gunney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Nadler, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Acids Encoded and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C64
; CURRENT APPLICATION NUMBER: US/09/989, 734
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR APPLICATION NUMBER: 60/091360  
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Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 246 GCGAGACCGGTATAGAGCGCTGCGCTTGGCCCGGACCGCAGGTTCCCGCGC 305  
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Db 1 GCGAGACCGGTATAGAGCGCTGCGCTTGGCCCGGACCGCAGGTTCCCGCGC 60  
;;  
QY 306 GCGCCGAGCCCCCGCGCC 323  
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Db 61 GCGCCGAGCCCCCGCGCC 78  
;;  
RESULT 27  
US-09-997-653-407  
;; Sequence 407, Application US/0997653  
;; Publication No. US2003008297A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnovers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Geiber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730PIC38  
;; CURRENT FILING DATE: 2001-11-15  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
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4 PRIOR APPLICATION NUMBER: 60/091519
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6 PRIOR APPLICATION NUMBER: 60/091626
7 PRIOR FILING DATE: 1998-07-02
8 PRIOR APPLICATION NUMBER: 60/091633
9 PRIOR FILING DATE: 1998-07-02
10 PRIOR APPLICATION NUMBER: 60/091978
11 PRIOR FILING DATE: 1998-07-07
12 PRIOR APPLICATION NUMBER: 60/091982
13 PRIOR FILING DATE: 1998-07-07
14 PRIOR APPLICATION NUMBER: 60/092182
15 PRIOR FILING DATE: 1998-07-09
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17 Query Match 24.1% Score 78; DB 11; Length 570;
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19 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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22 |||||
23 1 GCGAGAGCCGGGTATATAGAGCCTGTGCTTCCCGGCGAGCCGAGTTCCCGCGC 60
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25 QY 306 GCCCGAGGCCCGCGGCC 323
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27 Db 61 GCCCGAGGCCCGCGGCC 78
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29 RESULT 28
30 US-09-993-667-407
31 Sequence 407, Application US/09993667
32 Publication No. US20030022187A1
33 GENERAL INFORMATION:
34 APPLICANT: Ashkenazi, Avi J.
35 APPLICANT: Baker, Kevin P.
36 APPLICANT: Botstein, David
37 APPLICANT: Desnovers, Luc
38 APPLICANT: Eaton, Dan L.
39 APPLICANT: Ferrara, Napoleone
40 APPLICANT: Fong, Sherman
41 APPLICANT: Gerber, Hanspeter
42 APPLICANT: Gottard, Audrey
43 APPLICANT: Godowski, Paul J.
44 APPLICANT: Grimaldi, J. Christopher
45 APPLICANT: Gurney, Austin L.
46 APPLICANT: Kijavini, Ivar J.
47 APPLICANT: Napier, Mary A.
48 APPLICANT: Pan, James
49 APPLICANT: Paoni, Nicholas F.
50 APPLICANT: Roy, Margaret Ann
51 APPLICANT: Stewart, Timothy A.
52 APPLICANT: Tumas, Daniel
53 APPLICANT: Watanabe, Colin K.
54 APPLICANT: Williams, P. Mickey
55 APPLICANT: Wood, William I.
56 APPLICANT: Zhang, Zemin
57 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
58 FILE REFERENCE: P2730PLQ4
59 CURRENT APPLICATION NUMBER: US/09/993,667
60 CURRENT FILING DATE: 2001-11-14
61 PRIOR APPLICATION NUMBER: 60/049787
62 PRIOR FILING DATE: 1997-06-16
63 PRIOR APPLICATION NUMBER: 60/062250
64 PRIOR FILING DATE: 1997-10-17
65 PRIOR APPLICATION NUMBER: 60/065186
66 PRIOR FILING DATE: 1997-11-12
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70 PRIOR FILING DATE: 1997-11-24
71

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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 24.1% Score 78; DB 11; Length 570;  
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QY 306 GCGCGAGCGCCCGCGCGC 323  
DB 61 GCGCGAGCGCCCGCGCGC 78

RESULT 29  
US-09-997-428-407  
Sequence 407, Application US/09997428  
Publication No. US20030027162A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavyn, Ivar J.  
APPLICANT: Nadiet, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C44  
CURRENT APPLICATION NUMBER: US/09/997,428  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
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PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910

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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 11; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1,1e-09; Indels 0; Gaps 0;  
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QY 246 GCGAGACCGGGTATTAAGAGCTTCGTGCGCTTGCCTCCCGGAGCCGACGTTCCCGCGC 305  
DB 1 GCGAGACCGGGTATTAAGAGCTTCGTGCGCTTGCCTCCCGGAGCCGACGTTCCCGCGC 60  
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US-09-990-438-407  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
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; APPLICANT: Williams, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C3  
; CURRENT FILING DATE: 2001-11-14  
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/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

Query Match
Best Local Similarity 100.0%; Score 78; DB 11; Length 570;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCGAGGACCGGGATAGAGACCTCGGCGCTTGCCGCGGACGCGAGGTTCCCGCGGC 60

QY 306 GCGCGGAGCGCCCGCGCGCC 323
DB 61 GCGCGGAGCGCCCGCGCGCC 78

RESULT 32
US-09-990-562-407
/ Sequence 407, Application US/09990562
/ Publication No. US20030027985A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerlitsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gruney, Austin L.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2730P1C18
/ CURRENT FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: US/09/990,562
/ PRIOR FILING DATE: 1997-06-16
/ PRIOR APPLICATION NUMBER: 60/049787
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/ PRIOR APPLICATION NUMBER: 60/062250
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/ PRIOR FILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 11; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
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RESULT 33  
US-09-990-711-407  
; Sequence 407, Application US/09990711  
; Publication No. US20030032023A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyer, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerltzen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC2  
; CURRENT APPLICATION NUMBER: US/09/990, 711  
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PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 11; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;

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Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 246 GCGAGAGACCGGGTATAGAGCCTCGTGGCTTGGCCCGGACGCCGAGTTCCCGCGC 305
Db 1 GCGAGAGACCGGGTATAGAGCCTCGTGGCTTGGCCCGGACGCCGAGTTCCCGCGC 60
Qy 306 GCCCGAGCGCCCGCGCC 323
Db 61 GCCCGAGCGCCCGCGCC 78

RESULT 34
US-09-989-726-407
; Sequence 407, Application us/09989726
; Publication No. US20030040473A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Goddard, Audrey
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; APPLICANT: Tamas, Daniel
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TIME OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C60
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; PRIOR FILING DATE: 1997-06-16
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 11; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1,1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 306 GCGCGAGCCCGCGCGC 323  
Db 61 GCGCGAGCCCGCGCGC 78

RESULT 35  
US-09-998-156-407  
; Sequence 407, Application US/09998156  
; Publication No. US20030044806A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Guiney, Austin L.  
; APPLICANT: Klavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tomas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C28  
; CURRENT APPLICATION NUMBER: US/09/998,156  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/049787  
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Query Match 24.1%; Score 78; DB 11; Length 570;  
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QY 306 GCGCCGAGCCCCGCGCC 323  
Db 61 GCGCCGAGCCCCGCGCC 78

RESULT 36  
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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC49  
CURRENT APPLICATION NUMBER: US/09/990,437  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 11; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1,1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 306 GCGCGAGGCGCCCGCGCGC 323  
DB 61 GCGCGAGGCGCCCGCGCGC 78

RESULT 37  
US-09-991-157-407  
Sequence 407, Application US/09991157  
Publication No. US20030049638A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Goddard, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kijavitt, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C51  
CURRENT FILING DATE: 2001-11-16  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 11; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 GCGAGGACCGGATATAGAGCGCTTGCGCGGACAGCGGAGGTTCCCGCGCC 305  
Db 1 GCGAGGACCGGATATAGAGCGCTTGCGCGGACAGCGGAGGTTCCCGCGCC 60  
Qy 306 GCGCGAGCGCCCGCGGCC 323  
Db 61 GCGCGAGCGCCCGCGGCC 78

RESULT 38

US-09-997-514-407  
Sequence 407, Application US/09997514  
Publication No. US20030049681A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey E.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavits, Ivar J.  
APPLICANT: Majer, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Poni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C46  
CURRENT APPLICATION NUMBER: US/09/997,514  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 11; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GCGAGGACGGGATAGAGCCTCGGCGCTTGCCCGGAGCCGCGGAGTTCGCGCGC 305  
DB 1 GCGAGGACGGGATAGAGCCTCGGCGCTTGCCCGGAGCCGCGGAGTTCGCGCGC 60  
QY 306 GCGCGGAGCCCGCGCGC 323  
DB 61 GCGCGGAGCCCGCGCGC 78

RESULT 39  
US-09-997-573-407  
Sequence 407, Application US/09997573  
Publication No. US20030049682A1

GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deamoys, Luc  
APPLICANT: Ealon, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C45  
CURRENT APPLICATION NUMBER: US/09/997,573  
CURRENT FILING DATE: 2001-11-15  
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/ PRIOR FILING DATE: 1998-07-09

Query Match      24.1% Score 78; DB 11; Length 570;
Best Local Similarity 100.0%; Pred. No. 1,1e-09;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      246 GCGAGGACCGGGATTAAGAAGCTGTGGCTTGGCCGGGACGCGGATTTCCCGGCGC 305
DB      1 GCGAGGACCGGGATTAAGAAGCTGTGGCTTGGCCGGGACGCGGATTTCCCGGCGC 60
QY      306 GCGCCGAGCGCCCGGCGCC 323
DB      61 GCGCCGAGCGCCCGGCGCC 78

RESULT 40
US-09-991-172-407
; Sequence 407, Application US/09991172
; Publication No. US20030050457A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
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APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavitt, Ivan J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C50  
CURRENT FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: US/09/991,172  
PRIOR FILING DATE: 2001-11-16  
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PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR	FILING DATE:	1998-07-09

Query Match	24.1%;	Score 78;	DB 11;	Length 570;
Best Local Similarity	100.0%;	Pred. No. 1.1e-09;		
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			Indels	0;
			Gaps	0;

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Db	1	GCAGAGACCGGGATATAGAGAGCTGTGAGCCTTGC	CCCGGGGAGCGCGAGATTCCCCGAGC	60
Qy	306	GCCTCCGAGCTCCCGGAGC	323	
Db	61	GCCTCCGAGCTCCCGGAGC	78	

Search completed: November 6, 2003, 10:39:34  
Job time : 244.663 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 06:45:57 ; Search time 1862.61 Seconds  
(without alignments)  
4214.691 Million cell updates/sec

Title: us-10-081-817a-19\_COPY\_229\_551

Perfect score: 323 ggcgcgcggggcagaccgca.....ggcgcgcgcgcgcgcgcgc 323

Sequence: 1 ggcgcgcggggcagaccgca.....ggcgcgcgcgcgcgcgcgc 323

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 22781392 segs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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C 1	72.4	22.4	982 13	BX415111 BX415111
C 2	69	21.4	935 29	CNS006XK AL066051 Drosophila
C 3	64.6	20.0	526 9	AA742697 AA742697 nx30g04.8
C 4	64.6	20.0	1009 29	CNS010EW AL098882 Drosophila

Result No.	Score	Query Match Length	DB ID	Description
C 5	63.6	19.7	982 13	BX415111 BX415111
C 6	63.4	19.6	925 29	CNS0091P AL053013 Drosophila
C 7	63.2	19.6	1061 13	BX391246 BX391246
C 8	63.2	19.6	1203 29	CNS015Y4 AL106054 Drosophila
C 9	63	19.5	935 29	CNS006XK AL066051 Drosophila
C 10	61.8	19.1	932 29	CNS0072C AL066072 Drosophila
C 11	61.4	19.0	1057 13	BX349688 BX349688
C 12	61.4	19.0	1292 28	AZ673197 ENTLK77R
C 13	60.8	18.8	925 29	CNS0091P AL053013 Drosophila
C 14	60.4	18.7	1072 13	BX381336 BX381336
C 15	59.8	18.5	1144 13	BX415292 BX415292
C 16	58.6	18.5	840 29	AG053457 Pan t1091
C 17	58.6	18.5	1000 13	BX407619 BX407619
C 18	58.4	18.4	844 29	CNS0052P AL056652 Drosophila
C 19	58.4	18.4	1101 29	CNS01751 AL108460 Drosophila
C 20	58.3	18.3	703 29	AG054687 Pan t1091
C 21	58.8	18.2	1103 13	BX403654 BX403654
C 22	58.8	18.2	1581 29	AG052690 Pan t1091
C 23	58.4	18.1	932 29	CNS0072C AL066072 Drosophila
C 24	58	18.0	515 13	BX424977 BX424977
C 25	58	18.0	1201 29	CNS01523 AL106089 Drosophila
C 26	57.8	17.9	693 13	BX381320 BX381320
C 27	57.8	17.9	839 29	CNS004NB AL054280 Drosophila
C 28	57.8	17.9	881 13	BX368720 BX368720
C 29	57.6	17.8	910 29	CNS0060N AL056629 Drosophila
C 30	57.4	17.8	723 28	BZ046906 BZ046906
C 31	57.4	17.8	776 29	CNS010RY AL093352 Drosophila
C 32	57.4	17.8	1019 13	BO957113 BO957113
C 33	57.2	17.7	873 12	BG844318 BG844318
C 34	57	17.6	828 29	AG136798 AG136798
C 35	56.8	17.6	971 13	BO678466 BO678466
C 36	56.4	17.5	1126 13	BU185501 BU185501
C 37	56.4	17.5	1150 13	BO892481 BO892481
C 38	56.2	17.4	810 29	AG060267 AG060267
C 39	56.2	17.4	888 12	BG809572 BG809572
C 40	56	17.3	978 29	AG042900 AG042900
C 41	55.6	17.2	1030 29	AG126233 AG126233
C 42	55.6	17.2	1049 13	BO928358 BO928358
C 43	55.4	17.2	788 29	AG022923 AG022923
C 44	55.4	17.2	788 29	AG184464 AG184464
C 45	55	17.0	1076 12	BM479703 BM479703

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DEFINITION  
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ACCESSION  
BX415111  
VERSION  
BX415111.1  
SOURCE  
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ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Li, M.B., Gruber, C., Jesse, J., and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Genoscope  
Genoscope Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Web : www.genoscope.cns.fr  
Email: seqref@genoscope.cns.fr  
Library was constructed by Life Technologies, a division of Invitrogen, Contact : Feng Liang Email : fliang@litech.com URL : http://fulllength.invitrogen.com/invitrogen Corporation 1600 Paraday Avenue Genoscope sequence ID : CS0CAP004B5100P1.  
Location/Qualifiers  
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/organism="Homo sapiens"



/mol\_type="mRNA"  
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/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from 3 pooled  
germ cell tumors, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified p773  
vector. Library is normalized. Library was constructed by  
Bento Soares and M. Fatima Bonaldo."

BASE COUNT 88 a 162 c 189 g 85 t 2 others

Query Match 20.0%; Score 64.6; DB 9; Length 526;  
Best Local Similarity 83.9%; Pred. No. 0.0016; Mismatches 14; Indels 0; Gaps 0;  
Matches 73; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 237 GCTGAGAGGCGGAGACCGGTATAGAGCTTCGCTCCCGGACCGGAGGT 296  
DB 526 GCACGAGGCGCAGACCGGTATAGAGCTTCGCTCCCGGAGCGGAGGT 467  
QY 297 TCCCGGCGCGCGCGGAGCGCGCGCC 323  
DB 466 TCCCGGCGCGCGCGGAGCGCGCGCC 440

RESULT 4  
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LOCUS  
DEFINITION  
Drosophila melanogaster genome survey sequence SP6 end of BAC  
BACN03P19 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
AL098882  
GI:5610493  
GSS.  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 1009)  
Genoscope.  
Direct Submission  
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EMGP) -  
http://www.emgp.edb.ac.uk. This Drosophila melanogaster BAC  
library (Dros BAC) was made by Alain Billard at CERH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
Project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector  
peloBAC11.  
Location/Qualifiers  
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BASE COUNT 147 a 377 c 178 g 64 t 243 others

ORIGIN

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Best Local Similarity 37.4%; Pred. No. 0.0017;  
Matches 104; Conservative 64; Mismatches 103; Indels 7; Gaps 1;

QY 43 GGGCTTCGCGAGACAAAGCGCGGCTCTCTCTCAGAGGCGCCAGCGCTTGCCAG 102  
DB 964 GCGGCGGCGGCG 905

QY 103 AGGAAGTCTCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 162  
DB 904 CCGGCG 845

QY 163 CAGCAGGAAGTTGCG 222  
DB 844 CGACG 792

QY 223 CGGCG 282  
DB 791 CGACG 732

QY 283 GGGCG 320  
DB 731 GGGCG 694

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DEFINITION  
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5-PRIME, mRNA sequence.  
BX15111  
GI:30765470  
ACCESSION  
VERSION  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 982)  
L1.W.B., Gruber, C., Jessee, V. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/InvitrogenCorporation 1600  
Paraday Avenue Genoscope sequence ID : CS0CAP004BE100PL.  
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/db\_xref="taxon:9606"  
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/issue\_type="THYMUS"  
/clone\_1lb="Homo sapiens THYMUS"  
/note="Vector: pCMVSPORT.6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."

BASE COUNT 177 a 257 c 323 g 18 t 207 others

ORIGIN

Query Match 19.7%; Score 63.6; DB 13; Length 982;  
Best Local Similarity 34.2%; Pred. No. 0.0026;  
Matches 110; Conservative 69; Mismatches 144; Indels 0; Gaps 0;

QY 2 CGCGTGGGCTCAGACCGCAAGGAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 61  
DB 259 CCGCGGCG 318

QY 62 GCCGCGCGCTCTCTCTCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 121  
DB 319 GCGCGGCG 378

QY 182 GCACGGCCGCTGAGCGGAGCGGGCAGAGGCTTTCTCAGAGCGCGGGACGAGGCGCGCTG 241

Db 379 GGGGGSSSSGGGGGSSGGGGSMSSSSGGCCCCCGCCSSCGGGGSSCGSCSSGGGSGV 438

QY 122 GCGAGGGAAGGGGACACGGGCTTCCCGAGGGCCCGCGGCGCGACACAGAAATTGGACAG 181

Db 439 GGGSSSCGGCCSCSGSGSGSGGGGAGSSCCSSSGGGGCGCCCGCGGGSSCGGGSSGSSCS 498

QY 242 AGGGGAGAGAACCGGATTAAGAAACCTCTGAGCTTGGCCCGGACACCGCAGATTCCCC 301

Db 499 SGGGGGGGGGGGSSSGSSCGCCGAGCCCTCMGGGCGCCSCGSCSCCCCCCGGCCCCACAG 558

QY 302 GCGCGCCCGAGGCCCGCGGCC 323

Db 559 ACGGAGCCARCCSGAVAGSCS 580

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 925)	Genoscope.	Direct Submision	Submitted (02-jun-1999)	Genoscope - Centre National de Sequencage
			Submitted (02-jun-1999)	Submitted (02-jun-1999)
			BP 191 51006 EVRY cedex - FRANCE (E-mail : secrete@genoscope.cns.fr	
			- Web : www.genoscope.cns.fr)	
			Determination of this BAC-end sequence was carried out as part of a	

collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org>. The BDGP *Drosophila melanogaster* BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamonosher in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial *NotI* digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

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	120 a		511 others

Query Match	19.6%	Score 63.4	DB 29	Length 925
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Matches	44	Conservative 153	Mismatches 113	Indels 0
Gaps	0			
QY	1	GGCGGTGGGCTTCAGACCGCAAGCCGAAAGTGTGGGCGGGGTGGGCTTCGCGAGACAA	60	
	.....	.....	.....	
Db	867	SSSSGTSSACVCKCNASSCGCGCGGMBCCMCSSSSCTGSARARVKVPAAGAGAKRG	808	
	.....	.....	.....	
QY	61	GGCGGGGCTGTCTCTTCAGAGAGGCCCAAGCGCTCCCAAGAGAAATCTTCAGAGGCC	120	
	.....	.....	.....	

Dd	807	GAGGASASHSSSBACBSBSSSSCSASCWBSASSSSSASBSRBRGGGAAGSGASBSRSSSS	748
Qy	121	GGGCAGAGGAAAGGGGCGACGGGCTTCCCAAGGGCCGCCGCGCAGCAGAGAATTGGCCAG	180
Dd	747	SSASASASVVSASSSSSCSSSVSCSVASSMBCSBSSBSASASSSSSSSASACSCC	688
Qy	181	GGCACGGCCGTGACCGGACCGGCGACGGGCTTTCTCAGAGCGCGGCGAGCGCGCGCTG	240
Dd	687	CCTWSGCSTTSABWBAARSSSSSSSCSSSMASASSASASASSSSSSGSSSSSCAC	628
Qy	241	GAGGGGCGAGAACCGGGTTAAGAAAGCTTCGTGCGCTTGCCCCGGGACCGCAGTTTCCC	300
Dd	627	GBMSMSGGGGSVYSABSGMSVSSGRRSGSGGGGGVGSGSSGSSGSGSGSGSVCS	568
Qy	301	CGCGCGCCC	310
Dd	567	CSGCMCRCS	558

RESULT 7	EX391246	1061 bp	linear	EST: JJ-MAY-2001
LOCUS	EX391246			
DEFINITION	EX391246 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS00D1008YIN9.3-PRIME, mRNA sequence.			
ACCESSION	EX391246			
VERSION	EX391246.1			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			

REFERENCE  
1. (bases 1 to 161)  
AUTHORS Li, W. B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT Contact: Genoscope

Genoscope - Centre National de Séquençage  
BP 191 91006 EVRY cedex - France  
Email: [segre@genoscope.cns.fr](mailto:segre@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 7394.f. For  
more information about this cluster, see  
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSDBAH012ZH06NP1&cluster=7394.f>. Contact :  
Peng Liang Email : [liang@life-tech.com](mailto:liang@life-tech.com) URL :  
<http://fulllength.invitrogen.com/InvitrogenCorporation> 1600  
Faraday Avenue Genoscope/sequence ID : CSDBAH012ZH06NP1.

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FEATURES
    SOURCE
        1..1061
            location/qualifiers
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="CSOD1008YN19"
                /tissue_type="PLACENTA COT 25-NORMALIZED"
                /clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
                /note="1st strand cDNA was primed with a NotI-oligo(dT)
                primer. Five prime end enriched, double-strand cDNA was
                digested with Not I and cloned into the Not I and EcoR V
                sites of the pCMVSPORT 6 vector. Library was normalized."
    BASE COUNT
        225 a      153 c      229 g      209 t      165 others
    ORIGIN

```

Query Match	19.6%	Score 63.2;	DB 13;	Length 1061;
Best Local Similarity	29.5%	Pred. No. 0.0032;		
Matches	88;	Conservative	84;	Mismatches 126; Indels 0; Gaps 0

QY	3	GCCTGGGCTCAGACCGCAAGCGAAGGTGCCGGGCCGGGGCTTGC	CGGAGACCAACG	62
		.....		
Dy	294	GGBBVAGGTTNNNNSSBNNBSSSSGGGGGGSSGGSSGGSSGGGGG	GGGGGGGGG	353
QY	63	CCGGGCTTGCCTCTCTCAGAGGGGCCCGCCCTGCGACAGAGAA	GTCTTCGAGCCCGG	122
		.....		

Db	354	GSGGGGCGGCGGCAAGCGGCGGSGSGGCGGCGCGSSSSSGCGCGCGCGGCGGCGGSSSGGS	413
Oy	123	GCAGGAAGAAGGGCAGCGGCTTCCACAGAGCCCGCGCGCGAGAGAAATTGACACAGG	182
Db	414	GSGSGSGGCGCGGCGSSSGSSSGSGSGSGSGSGSGSSSXXKXGSSSXSSSGCGSS	473
Oy	183	CACGGCGGTGAGCGAGCGCGGCGGCTTTTCAGAGAGCGCGGCGACGCGGCGCTGGA	242
Db	474	SAGGCGGSGSGGCGGSGCGCGCGGSSSSBSKXSQCSGCGCGCGCGGCGGSS	533
Oy	243	GGGCGCGAGACC GGCTTAAGAACCTTGCTGCTTCCCGCGGCGACGCCAGTTCCC	300
Db	534	GGGGGAGSGGSSGSGGSGGCGGCGCGGCGGAGCGAGKXSGGSCGSSCGSGGCGGCGCC	591
RESULT 8			
CNS015Y4			
LOCUS			
DEFINITION	CNS015Y4	1203 bp	linear GSS 26-JUL-1999
ACCESSION	Drosophila melanogaster genome survey sequence T7 end of BAC		
VERSION	BACN15E10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.		
KEYWORDS	AL106054		
SOURCE	AL106054.1 GI:5619805		
ORGANISM	Drosophila melanogaster (fruit fly)		
AUTHORS	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Empidoidea; Drosophilidae; Drosophila. 1 (bases 1 to 1203) Genoscope. Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk. This Drosophila melanogaster BAC library (Dros-edgp.ebi.ac.uk) was made by Alain Billard at CSH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector peloBAC11.		
COMMENT			
JOURNAL			
FEATURES			
source			
Location/Qualifiers			
1..1203	/organism="Drosophila melanogaster"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:7227"		
	/clone="BACN15E10"		
	/clone_1ib="DrosBAC"		
	/plasmid="peloBAC11"		
	/note="end : 77"		
BASE COUNT	154 a 274 c 380 g 158 t 237 others		
ORIGIN			
Query Match	19.6%; Score 63.2; DB 29; Length 1203;		
Best Local Similarity	35.7%; Pred. No. 0.0032;		
Matches 115; Conservative 72; Mismatches 133; Indels 2; Gaps 1,			
Oy	2	CGGCTGGGCTCAGACCGCAAAGCGAAGTGGCGGCGCGGATGGCGCTCGCGAGCAAG	61
Db	877	CGCGGGGCGSSCGCSSSGCGSGSGGGGGGGGGGGGAGCGGCGGAGVSSGSGGVVG	936
Oy	62	GCGGCGCGCTTCTCTCAGAGGGCCCCAGCGCTTCGACAAGAAATCTGAGGCCG	121
Db	937	VWVGSGSMGAGVGAIVAGGGGAMSCMGVSSSVSSGSSSGGGCGGSSSGCGGGVGG	996
Oy	122	GCGAGGAAGGGGCGACGGGCTTCCAGAGCCCGCGCGCGCACAGAAATTGGCGAG	181
Db	997	CGVWGgg--GGGGGCCSSSGSGGAGMGMNMGGGGGAGMSGGGSSSSGGGGGGGGGG	1054
Oy	182	GCAAGCGCTTAGCGGAGCGGCGCGGCTTTCTCAGAGCGCGGCGCGAGCGCGCTGG	241

[illegible]

[illegible]

RESULT	10
CNS00720	
LOCUS	932 bp DNA linear GSS 03-JUN-1996
DEFINITION	Drosophila melanogaster genome survey sequence IT end of BAC # BACttA809 of RPCI-98 library from Drosophila melanogaster (fruit fly) genomic survey sequence.
ACCESSION	AL066742
VERSION	AL066742.1
KEYWORDS	GI:4945205
SOURCE	GSS.
ORGANISM	Drosophila melanogaster (fruit fly) Drosophila melanogaster Drosophila melanogaster

REFERENCE 1 (bases 1 to 932)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage

COMMENT  
Determination of this BAC-end sequence was carried out as part of a

Arnon Memmoser, in Pieter de Jong's laboratory in the Department of Cancer Genetics, at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BGP from the isogenic strain Y2, on bw sp. the same strain used for the BGP's and BSN. Interestingly, a more detailed description of the library and filters for hybridization from the BACP Resource Center can be found at <http://bacpac.med.buffalo.edu/drosophila/bac.htm>.

```

* SOURCE
1. .932

```

BASE COUNT	155 a	202 c	241 g	91 t	243 others
ORIGIN					

Query Match	19.1%	Score 61.8	DB 29	Length 932
Best Local Similarity	13.6%	Pred. No. 0.061		
Matches 102	Conservative 77	Mismatches 144	Indels 0	Gaps 0

QY	1	GGCGGAGGAGTCAAGCCGCAAGCGAAGTCTCGGCGCGGAGTGGGCTTCGCGAGACAA	60
Db	609	GGSCRGGGGGGCGCGSGGCGCGGSSCGSCGCGGSGAGCCCGCGCGSSGCGSSGCG	668
QY	61	GGCGGAGGCTGCTCTTCACAGGAGCCCGACAGCGCTTCGCAAGAGGAAGTCTTCGAGGCCC	120
Db	669	SGSGSGGCGCGGSSGCGCGCGCCSSGCGSCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	728
QY	121	GGGCGAGGAGAGGGGCGACGCTTCCACAGGCGCCGCGCGCGGACGACGAGAGATTGGCCG	180

[illegible]

RESULT 11	
LOCUS	EX349688
DEFINITION	EX349688 Homo sapiens P1ACNTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION	EX349688
VERSION	EX349688.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)

REFERENCE	1 (bases 1 to 1057)
AUTHORS	K4,W.B., Gruber,C., Jesssee,J. and Playates,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
COMMENT	Contact: Genoscope

BP 191 91006 EVRY cedex - France

```

FEATURES
  source
    cg1-103n1.cluster.cgi?seq=C50BAH015ZB03NP1.1&cluster=7092.r. Contact :
    Feng Liang Email : liang@life.technic.com url :
    http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
    Paraday Avenue Genoscope sequence ID : C50BAH015ZB03NP1.
    location/Qualifiers
      1.103n1
      organism="Homo sapiens"
      mol_type="mRNA"
      db_xref="taxon:9606"

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/tissue type="PLACENTA COT 25-NORMALIZED"
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## ORIGIN

[illegible]

[illegible][illegible]

Db 557 SSSGSSSSSSSSSYTTAKSTASAGSGWSAGGSGSGTGSTSSSSSSSSSTSTSSSSSVSSGSK 716

Qy 122 GGAGAGGAGAGGGGCGACGGGCTTCCACGAGCCGCGCGCCGACGAGAAATTGGCCAG 161

Db 717 SSTRBSSGSBSSSSSSSSSSSTSBBSCTTSSSSSSSSSVSSSTCSCTTCCCTSYSSSTSS 776

Qy 182 GCACGGCCGTGAACGGAGCGGCGAGGCTTTCTCAGAGACGGGGCGAGCCGCGCTGG 241

Db 777 SSTGWSGSTSSSSSSSVTSSSSBDSSTSTCCSCCYCTCCSTYBMCYTSSTCGSSSSSG 836

Qy 242 AGGCGGAGAGACCGGGTATPAGAACGCTGTGGCTTCCCGGAGCCGACGATTTCCC 301

Db 837 KGGVTCKCGCGCGSSSTTGMBSATCASSSSSSCGSSSVSSSKSBAASSSVSSGSGV 896

Qy 302 GCGGCGCCCGAGGCTCCC 319

Db 897 SSNSSSASKSSSSGSVSS 914

RESULT 14	LOCUS	DEFINITION
EX381336/c	1072 bp	mrna linear EST 08-MAY-2003
EX381336		EX381336 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
		clone CS0D1064YA14 3-prime, mRNA sequence.

ACCESSION	BX381336
VERSION	BX381336.1
	GI:30452937

SOURCE ORGANISM	Homo sapiens (human)

REFERENCE  
1 Mammalia; Eutheria;  
1 (bases 1 to 1072)

**TITLE** Full-length cDNA lib

**JOURNAL** Unpublished

CONTACT: GENOSCOPE  
Genoscope - Centre N  
BP 191 91006 EVRY ce

Email: [segre@genoscope.cns.fr](mailto:segre@genoscope.cns.fr), Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 674.r For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSVD1064BA07NP1&cluster=674.r>. Contact : Feng Liang Email: [liang@litech.com](mailto:liang@litech.com) URL: <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSVD1064BA07NP1.

FEATURES  
SOURCE

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDD1064YA14"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_1fb="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI primer. Five prime end enriched, double-stranded digested with Not I and cloned into the Not I sites of the pCMVSPORT 6 vector. Library was 1
172 a 324 c 268 g 231 t 77 others
BASE COUNT
ORIGIN

```

Query Match	18.7%	Score 60.4	DB 13	Length 1072
Best Local Similarity	44.7%	Pred. No. 0.012		
Matches 122; Conservative		Mismatches 127	Indels 0	Gaps 0
QY	23	GGCAAGTGTGGGGCGGGGCTTCCGGAGACAAGGCGGGCGTGTCTTCACAA	82	
	1021	GGGCGGGGGGGGGGGCGGGGGCGCGCGAGGCGGGGGGGGGCGCGGGGGGGCGG	962	
QY	83	GGGCGCCGACGGCTTCCCAAGAGAGAGTCTTCGAGGCGCCGGGCGAAGGGGCGACGGGC	142	

[illegible]

RESULT 15  
PY41E936

LOCUS	1144 bp	mRNA	linear	EST 13-MAY-2003
DEFINITION	BX415926 Homo sapiens	CDNA	clone CS0CAP008YH01	

ACCESSION	BX415926	
VERSION	BX415926.1	GI:30650131

SOURCE ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE  
1 (bases 1 to 1144)  
Lammaliya; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homininae; Hominini; Homo

Full-length cDNA libraries and normalization

COMMENT:  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 101 01006 Evry Cedex - France

Email: [segreff@genoscope.cns.fr](mailto:segreff@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by Life Technologies

more information about this cluster, see <http://www.genoscope.cns.fr/>

FEATURES  
cgis\_bin/cluster cgiseg=CS0CAP008CD01Q8C1cluster=9916.f. Cont  
Feng Liang Email : fliang@lietech.com URL :  
http://fulllength.invtbrogem.com/ Invtbrogem Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0CAP008CD01Q81.  
Location/Qualifiers

Source

```

/mo1_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP008YH01"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/notes="Vector: pCMVSORT 6; 1st strand cDNA was primed
with a NotI-oligo (dfr) primer. Five prime end,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSORT 6 vector.
Library was not normalized."

```

Query Match	18.5%;	Score 59.8;	DB 13;	Length 1144;
Best Local Similarity	35.6%;	Pred. No. 0.015;		
Matches 115;	Conservative	58;	Mismatches 150;	Indels 0;
				Gaps 0;

QY 1 GCGCGTGGGGGTCAAGCCGCAAGCGAAGATGTCGGGCGCGGGGTGTGGGCTTCGCGAGACAA 60  
 Db 794 GGGGGGGGGCGCGGGSSSGCGGGGGGSCSCGCGCGGGGGGGSSGCGSSGSGSGS 853  
 QY 61 GGC CGCGGCTGTCTTCTTCAGAGGCGCCCAAGCGCTCTCCAAAGAGAAGTCTTGAAGGCC 120  
 Db 854 GGGCGGSGSGGSGCGGCGCGCGCGGCGCCSGGGGGGGGGGCGGCGCGCGCGGGGCS 913  
 QY 121 GGGCAAGGAGGGGGGCAAGGCTTCCAGAGGCCCGCGCGGCGCAGCAGAGATTGGCCAG 180



[illegible]

## RESULT 16

LOCUS	AG0043467	940 bp	DNA	linear
DEFINITION	Pan troglodytes DNA, clone: FTB-021M16.F, genomic survey sequence.			
ACCESSION	AG0043467			
VERSION	AG0043467.1	GI:16572192		
KEYWORDS	GSS.			
SOURCE	Pan troglodytes (chimpanzee)			
ORGANISM	Pan troglodytes			

REFERENCE AUTHORS	TITLE	JOURNAL	REFERENCE AUTHORS	TITLE	JOURNAL
1	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.	BAC end sequences of library PTB	2	Unpublished	
			2	(Passes 1 to 840)	
	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.			Direct Submissions	
	Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical				

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
E-mail: chumpo@ssc.riken.go.jp, URL: <http://hsp.gsc.riken.go.jp/>,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the RAD process and may have higher chance of  
clone tracking errors.  
PRIMERS

```

LIBRARY
  Vector      : PKSI45
  R.Site 1    : Saci
  R.Site 2    : Saci
  Location/Qualifiers
    1. 840

```

```

/ol type="genomicDNA"
/db xref="taxon:9598"
/clone="PTB-021M15.F"
/sex="male"
/cell_type="lymphoblast"
/clone_11b="PTB Chimpanzee Male BAC Library"
57 a 332 c 397 g 14 t 40 others

```

[illegible][illegible]

RESULT 17  
PY407619

LOCUS	BX407619	1000 bp	mRNA	linear	EST 15-MAY-2003
DEFINITION	BX407619	Homo sapiens	PLACENTA	Homo sapiens	CDNA clone CS0DE005Y119
ACCESSION	BX407619				
VERSION	BX407619				
KEYWORDS	5-PRIME, mRNA sequence.				
EST.	BX407619.1	GI:30762809			
SOURCE	Homo sapiens (human)				

REFERENCE  
Eklavtaya, I.; Metherzaa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1000)  
Li, W. B., Gruber, C., Jesses, J. and Polyes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Genoscope [Walter@Genoscope.fr](mailto:Walter@Genoscope.fr)

BP 191 91006 Evry cedex - France  
Email: [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 6789.f For  
more information about this cluster, see  
[http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0A0053D02Q2P1&cluster=6789.f](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0A0053D02Q2P1&cluster=6789.f). Contact :  
Feng Liang Email : [liang@litesattech.com](mailto:liang@litesattech.com) URL :  
<http://fulllength.invitrogen.com/InvitrogenCorporation1600>  
Fairday Avenue Genoscope sequence ID : CS0A0053D02Q2P1.

```

source
1, 1000
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="Gene,9606"
/cdate="CSDB0503119"
/cisue_type="PLACENTA"
/cisue_tlib="Homo sapiens PLACENTA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-Oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector."

```

BASE COUNT	226 a	205 c	283 g	57 t	229 others
ORIGIN					
Query Match		18.5%	Score 59.6;	DB 13;	Length 1000;
Best Local Similarity		23.4%;	Pred. No. 0.017;		
Matches	60;	Conservative 102;	Mismatches	94;	Indels 0;
					Gaps 0;

Qy 2 CGCGGGGTCAGACCGCAAGCGCAAGTCCGGGCGCGGGTGTGGGCTCGCGAGCAAG 61  
 Db 431 CMSCCGGSGSGAGVCSGGGGGGGGGGVMAAGGGGCGCCSGGGGGGGGGGGGGGR 490  
 Qy 62 GCCGGGCTGACTCTCTCAGAGAGGCCCAAGCGCTTCGCAAGAGAGATCTCAGAGCCG 121  
 Db 491 RSSGGGCGSGAGSCCSGGGGGAGCTCWCSSSSGGGCGGAGSSGSGSGSGSSSSS 550

Qy	122	GCGAGGAAAGGGG	CACGGGCTTCC	AGGGCCCCGGCC	GACACAGGAATTGG	CAAG	181
Db	551	SSSSSSSSSV	SVSSSVSSSSSSSS	SSSSSSSR	ASSSSSSSV	RVVVAAVA	VSSGSS
Qy	182	GCACGGCCCT	GAAGCGGAGCGG	AGGCTTTCT	CAGACCGCGG	CGACCGCCCT	GTG
Db	611	GSSGAAAGGSS	SGSSSSSSSSSSSS	SSSSSSSG	SSSSSSSG	SSSSSV	GSSSSAGGG
Qy	242	AGGGCGCAG	AGACCGGG				257
Db	671	GGGGG	GGGGGGGGGG				686

RESULT 18					
CNS0052p					
LOCUS	844 bp	DNA	linear	GSS 03-JUN-1999	
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC #				
	BACRIAP6 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL056652				
VERSION	AL056652.1				
KEYWORDS	GI:4932342				
SOURCE	GSS.				
ORGANISM	Drosophila melanogaster (Fruit Fly)				

REFERENCE	1 (bases 1 to 844)
AUTHORS	Genoscope.
TITLE	Direct Submision
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage

**COMMENT**

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oosagawa and Aaron Mamoser. In Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES	
source	location/Qualifiers
1..844	location= "Drosophila melanogaster"
	mol_type= "genomic DNA"
db_xref= "taxon:7227"	
clone= "BACR11p16"	
clone_11b= "RPC1-98"	
/note= "end: TET3"	
261 a	112 c 92 g 35 t 344 others
BASE COUNT	
ORIGIN	

	Query Match	Similarity	Score	DB	Length
	Best	Local			
	Matches	Conservative	132	Mismatches	91; Indels 0; Gaps 0;
QY	1	GGGCGTGGGGTCAGACCGCCAAAGGACGTGCGGGCGGGGTGGCGCTCGCCGACAA	60		
Db	417	SCGSSGSSSCAMSSCCCTVSSCGMASSSCCGGASASSSSGGVSSVSGRIVVGRGR	476		
QY	61	GGCGCGGCGCTGCTCTCTCAGAGGGCCCGCAGCGCTCCAGAGAACTCTCGAGGCCC	120		
Db	477	CMCGSMVCCCMCCSMCCSVBSVCAVCSGSVSVAVGCGVGRVGGSSRRGAHSS	536		
QY	121	GGGCGAGGAAGGGGCGACAGGGCTTCCAGGGCCCCCGCGCGACGAGAAATTGGCCAG	180		

Db	53	GRGGSSSVSSGVVSSSSSVGMGCACASASVSCSSSVASSSVSSGBVSRGCGRCVGGGTVG	59
Qy	181	GGACGGCCCTGTATGACCGGACGGGACGGAGGCTTCTCAGAGCGCGCGAGAGCCCGCCCTG	24
Db	597	GGSRVSCSSGSSSSSSSCGCSVSSRRGSGANGVYVGGSGRRGGCGGGRGSGANAPADD	65
Qy	241	GAGGGCGAGACCGGCTTAAAGACCTTCG	271
Db	657	AAABRABKAPANSNADAPAAVSSSVSSBG	687

RESULT 19	
CNS0175Y	
LOCUS	CNS0175Y
DEFINITION	CNS0175Y 1101 bp DNA linear GSS 26-JUL-1998
ACCESSION	Drosophila melanogaster genome survey sequence S6 end of BAC BACN27L08 of DrosBAC library from Drosophila melanogaster (fruit fly) genomic survey sequence.
VERSION	AL108460
KEYWORDS	AL108460.1 GI:5628764
SOURCE	GSS.
ORGANISM	Drosophila melanogaster (fruit fly)

REFERENCE 1 (bases 1 to 1101)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage

**JOURNAL**  
Submitted (23-JUL-1999) Genoscope - Centre National de Séquençage  
BP 191 91006 EVRY cedex - FRANCE (E-mail: seque@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of  
collaboration with the European Drosophila Genome Project (EDGP) -  
<http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC  
library (Dros BAC) was made by Alain Billand at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MC  
Project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector  
pBeloBAC11.

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FEATURES
  source
    location/Qualifiers
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        /clone_11b="DrosBAC"
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        /note="end : SP6"
BASE COUNT
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ORIGIN

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Best Local Similarity	16.7%	Pred. No. 0.0	Matches	0
Matches	50	Conservative 143	Mismatches 106	Indels 0
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Db	676	GKKAKGTGRRGVCCAGAGGAGCACMAADCGCCAKYACSSSASBSGSCASTSSASR	735	
QY	83	GGGCCCCAGCGCTTGCCAAAGAGAAATCTTGAGCGCCGGGACAGGAGGGGCGACGGCC	142	
Db	736	GGMTVSSCCAGSGSGSGAGSACASAGAGGSGSGRGGSGCCASGYCGAACSSASCSMSG	795	
QY	143	TTTCCAGGAGCCCGCGCGCGCAGCAGAGGAATTGGCCAGGCGACAGCGCGTGTAGCGAGCG	202	
Db	796	VSSGSSCSAGSCGCGVSSCGAVSASASVMSYKAVASCSAVASGMAVSSBCHS	855	
QY	203	GGAGGAGCTTTCACAGACCGCGGGCGAGCGCGCGCTGAGGAGGGGCGCAGACCGAGATTA	262	
Db	856	SVTASVSAAASVSSSVSSSSSVVSAALVABSSSAASMTAVAAAAAVASVSVA	915	
QY	263	GAAAGCTGTGGCTTGCGCGGAGCGCAGGTTCCCGCGCGCCCGAAGCCCCGCG	321	

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Db          916  VSSSSSCSSSSASVYVASVAASASVSSSSSSSVSTSSASVSVASVMSAVVSS 974
RESULT 20
LOCUS       AG054687              703 bp    DNA             linear    GSS 02-NOV-2001
AC0054687
Pan troglodytes DNA, clone: PTB-040H03.F, genomic survey sequence.
DEFINITION  AG054687
AC0054687
VERSION     GI:16592130
KEYWORDS
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM    Pan troglodytes
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE   1
            Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
            Totoki, Y., Watanabe, H. and Sakaki, Y.
            BAC end sequences of library PTB
            Unpublished
            2 (bases 1 to 703)
            Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
            Totoki, Y., Watanabe, H. and Sakaki, Y.
            Direct Submission
            Submitted (02-NOV-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
            1-7-22, Suhrtsu-chou, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
            E-mail: chimpesegsc.riken.go.jp URL: http://hsp.gsc.riken.go.jp/,
            Tel: +85-503-9111, Fax: +81-45-503-9170
            Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the Rad process and may have higher chance of
            clone tracking errors.
            PRIMERS
            Sequencing: -21M13
LIBRARY
            Vector      : pKS145
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            R.site 2    : SacI.
            Location/Qualifiers
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                /cell_type="Tlymphoblast"
                /clone_1lb="PTB Chimpanzee Male BAC Library"
BASE COUNT  51 a          254 c          369 g          16 t          13 others
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Query Match      18.3%; Score 59; DB 29; Length 703;
Best Local Similarity 52.6%; Pred. No. 0.022;
Matches 154; Conservative 0; Mismatches 135; Indels 4; Gaps 14.
Db          91
QY          91  GCGCCGCAAGAGAGAACTCTCGAGCGCCCGGAGAGGAGGACACGAGCTTCCAG 150
Db          329  GGGCCCCCGACCGCGCCCCCGGCGCGCCCCCGGGGGGGGGGGCGCGGCGCGCG
QY          151  GCGCGCGCGCGCGAGAGAAATTGGCGCAGGGGCAACGCGCGTAGAG---CGAGACGGGCGAG 206
Db          389  GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGCGCGGGGCGCGGAGCGCCGCAAGCGCG 448
QY          207  GGGCTTCTCAGAGAGCGCGGGCGAGGCGCGGCTGAGAGGGCGAGAGACCGAGTAAAGAG 266
Db          449  GGGGGGGCGCGCGCGCGCGAGCGCGCGCGCGCGCTCGCGCGCGCGCGCGCGCGAGACAG 508
QY          267  CCTCGTGGCTTTCGCGGGCAGCGCAGAGTTCCCGCGCGCGCGCGAGCGCCCG 319
Db          509  CGCGCGCGCGCGCGCGCGCGCGCGGATCGAGCGCGCGCGCGCGCGCGCGCGCG 561

```

[illegible]

REFERENCE	TITLE	JOURNAL	AUTHORS	ORGANISM	SOURCE
1	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Toriki, Y., Watanabe, H. and Sakaki, Y.	BAC end sequences of Library PTB unpublished	2 (bases 1 to 1581)		
2	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Toriki, Y., Watanabe, H. and Sakaki, Y.	Direct Submission	Submitted (02-AUG-2001)		
3	Asano Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22, Suhrincho, Tsukuba, Ibaraki, 305-8565, Japan				
4	E-mail: chimp@gscc.riken.go.jp, URL: http://hnp.gscc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170				
5	Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.				
6	PRIMERS				
7	Sequencing: M13rev				
8	LIBRARY				
9	Vector : pKS145				
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11	R.Site 2 : SacI.				
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13	1. 1581				
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16	/db_xref="taxon:9598"				
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18	/sex="male"				
19	/cell_type="lymphoblast"				
20	/clone_id="PTB Chimpanzee Male BAC library"				
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23	ORIGIN				
24	Query Match				
25	Best Local Similarity 18.2%, Score 58.8, DB 29, Length 1581;				
26	Matches 147; Conservative 46.2%; P-Id. No. 0.024; Mismatches 171; Indels 0; Gaps 0;				
27	1 GCGCGTGGGTCAGACCCGCAAGCGAAGTGGCGCGCGGCTTCGCGAGACAA 60				
28	271 GAGCGCGCGGGGCGGGGCGGAGCGGGCGCGGCGGCGGCGGCGGCGGCGG 330				
29	61 GCGCGGCGCTTCCTTCAGAGGGCGCGCGCGCGCTTCGCAAGAGAACTTCAGAGCC 120				
30	331 GCG 390				
31	121 GCGCGAGGAGAGGGGCGCGCGCTTCAGAGGGCGCGCGCGCGCGCGAGAGAAATTGGCCAG 180				
32	391 GNGCGCGGAGGAGGCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 450				
33	181 GCGAGCGCGCTTCAGAGCGGCGCGCGCTTCCTCAGAGAGCGGGCGAGCGCGCGCTG 240				
34	451 GCG 510				
35	241 GAGGCGCGAGAGCGCGGATTAAGAGCGCTCGAGGCTTCGCGCGCGAGCGCGAGTTGCC 300				
36	511 GNGCGCGGAGGCGG 570				
37	301 GCG 318				
38	571 GCG 588				
39	RESULT 23				
40	CNS00720/c				
41	LOCUS				
42	DEFINITION				
43	CNS00720 932 bp DNA linear GSS 03-JUN-1999				
44	Drosophila melanogaster genome survey sequence T7 end of BAC #				
45	BAC14809 of RP11-98 library from Drosophila melanogaster (fruit				

ACCESSION  
 AL066742.1 GI:4945205  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Drosophila melanogaster (fruit fly)  
 Drosophila melanogaster  
 Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota;  
 Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha;  
 Ephyridiidae, Drosophilidae, Drosophila.  
 1 (bases 1 to 932)  
 Genoscope.  
 Direct Submission  
 Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage :  
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqret@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila  
 melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org/TheBDGP/Drosophila>  
 melanogaster BAC library was prepared by Kazutoyo Oosawa and  
 Aaron Mammosses in Pieter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPCL-98 and was constructed by partial  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 isogenic strain Y2; cn bw sp. the same strain used for the BDGP's  
 P1 and EST libraries. A more detailed description of the library  
 and how to order individual BAC clones, the entire library, or  
 filters for hybridization from the BACPAC Resource Center can be  
 found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).  
 location/Qualifiers  
 1 932  
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 /clone="BACR14B09.98"  
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 BASE COUNT 155 a 202 c 241 g 91 t 243 others  
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 Match Local Similarity 34.5%; P-adj. No. 0.029;  
 Matches 102; Conservative 70; Mismatches 121; Indels 3; Gaps 1;  
 Oy 28 GGTGCGGAGCCGGGCTGGGCTTCGCGAGACAAAGCCGGGCTGCTTCTCAGAGGCC 87  
 Db 918 GCGCGSSSSCGGSGSGCGSSCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 859  
 Oy 88 CCAAGCGCTCTCAAGAGAGAGTCTTCAAGAGCCCGCGGCGAGAGAGGAGCGAGCGCTTCC 147  
 Db 858 CGSSGSGCGCCCGCGSGSGGCGCCSSGSGSSCGSSGCGSSCGSSCGSSCGSSCGSS 799  
 Oy 148 AGGCGCCCGCGCGCGCGCGAGCAAGATTGGCGCAAGGCGCGCGCTGAGCGAGAGGGCGCAG 207  
 Db 798 CGCGSSSSCGSCCG 739  
 Oy 208 GCTTCTCAGAGAGCGCGGCGGAGCGCGCGCGCTGAGAGAGGCGAGAGCGGAGTAAAGAAC 267  
 Db 738 GG---GSSGSGSGCGSSGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 682  
 Oy 268 CTGCTGCGCTTGGCGCGGCGCGAGCGAGGTTCCCTCGCGCGCGCGCGCGCGCGCG 323  
 Db 681 SGCGGSGCGSCG 626

KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 515) Li, W.B., Gruber, C.E., Jesssee, J., and Polayes, D. Full-length cDNA libraries and normalization unpublished Contact: Genoscope Genoscope Centre National de Sequencage BP 191 91006 EVRY cedex France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6304.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CL0BA005ZH04.f&plicluster=6304.f. Contact : Feng liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CL0BA005ZH04.fpl. location/Qualifiers 1..515
FEATURES	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CL0BA005ZH04" /tissue_type="PLACENTA" /clone_id="Homo sapiens PLACENTA" /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
BASE COUNT	44 a 22 c 56 g 173 t 220 others
ORIGIN	
Query Match	18.0%; Score 58; DB 13; Length 515;
Best Local Similarity	8.3%; Pred.No.0.034;
Matches	17; Conservative 116; Mismatches 59; Indels 0; Gaps 0;
Oy	131 GGGGCGACGGAGCTTCACAGGGCCGCCGCACAGAAATTGCCAGGCGACGGCCC 190
Dd	323 GGGGGCGSSSSSVSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSAAMAA 382
Oy	191 TGAGCGAGCGGGCAGGGCTTTCTTGAGAGCCGGCGGCGAGCGCGGTGAGAGGGCGAG 250
Dd	383 AAAAAAASSGA 442
Oy	251 GACC GGATATAAGAAGCCTCTGAGCGCTTGCCCGCGCACCGCAGAGTTCCCGCGGCCCC 310
Dd	443 NANNNNNANNNNNSGNNGSSSSSSSSSSSSSSSSSSSSSSSVAAAASSSSSSSSSSSSSSS 502
Oy	311 GAGCCCCCGCGC 322
Dd	503 SSGSSSSSSSSSS 514
RESULT 25	CNS015Z3 1201 bp DNA linear GSS 26-JUL-1999
LOCUS	Drosophila melanogaster genome survey sequence Sp6 end of PAC
DEFINITION	BAC13106 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL106089.1 GI:5620019
VERSION	GSS.
KEYWORDS	Drosophila melanogaster (fruit fly) Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Empidoidea; Drosophilidae; Drosophila. 1 (bases 1 to 1201)
REFERENCE	

**AUTHORS**  
Genoscope.  
**TITLE**  
Direct Submission  
**JOURNAL**  
Submitted (23-JUL-1999) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

**COMMENT**

- Web : www.genoscope.cns.fr  
- Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelosBAC11.

**FEATURES**  
**Source**  
location/Qualifiers  
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    /note="end : Sp6"

**BASE COUNT**  
177 a         221 c         279 t         202 others

**ORIGIN**

Query Match	18.0%; Score 58; DB 29; Length 1201;
Best Local Similarity	36.0%; Pred. No. 0.035;
Matches 116; Conservative %58; Mismatches 148; Indels 0; Gaps 0;	

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Qy      2 CGCCTGGAGGTTCAGACCCGCAAAAGCGAAGTGCAGGCCGCGCGGTTGCCTTCGCGAGACAAG 61
Db      840 CVGAAGGGGAGGAGMGMMAMGAMGGGGGGGGGGGGGGCGCGSCRMAGAAAAAAMVVG 899

Qy      62 GCCGGGGCTGCTCTTCAGAGGGCCCCAGGCGCTGCCAAGAAGAATCTTCGAGGCCG 121
Db      900 VGGGMSMCRACMGCGGGGGGGGASCCCTCCVCASGMGRAYVVSgyRGSGSGSSCSGCC 959

Qy      122 GGCAAGGAGAGGGGCAAGGCTTCCAGAGGCGCGCGCGCGCACAGAAATTGGCCAG 181
Db      960 GCGGSCCGSCCGCCSCSGCGGCGRGSVMCRGCGCGCGSCGCGGGGGGGGGCGGG 1019

Qy      182 GCACGCGCTGTAGCGGAGCGGCGAGGGCTTTCTCAGAGCGCGGCGCACAGCGCCGCTGG 241
Db      1020 GGGGGGGGCGCGGGGAGGGGGGCGGSGGSGGSGGSSSCGASCAGCGGGCGGCGCGCG 1079

Qy      242 AGGGGCGAGAGCGCGGTAATAAAGCTCTGTGCCTTGCCCGGGCAGCGCAGATTCCC 301
Db      1080 GGGGSGGGGGCGCCCTCSSASAGCGCGCGGSGGSGGSGCGCGCGVSGCGSCGACCGSGCG 1139

Qy      302 GCGGCGCCCGAGCGCCCGCGGCC 323
Db      1140 GGGSCACGSGGGSGCGGGSGGCG 1161

RESULT 26
BX381320/c
LOCUS
DEFINITION
ACCESION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Genoscope - Centre National de Sequençage
BP 191 91006 EVRY cedex - France

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http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Paradise Avenue Genoscope sequence ID : CS0BAE021ZA02\_AE01930\_1.  
Location/Qualifiers

1. .881

FEATURES  
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/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT  
ORIGIN

37 a 147 c 355 g 65 t 277 others

Query Match 17.8%; Score 57.8; DB 13; Length 881;  
Best Local Similarity 48.8%; Pred. No. 0.038;  
Matches 143; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 31 GCGGGCGGGGTGGGCTCGCGAGACAAAGCGGCGCTCTCTGAGAGGCCCA 90  
DB 552 GGG 611  
QY 91 GCGGCTGCCAAGAGAGTCTCTGAGGCGCGGAGGAGGAGGAGCGGCTTCCAG 150  
DB 612 GGG 671  
QY 151 GCGGCGCGGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 210  
DB 672 GGG 731  
QY 211 TTTCAGAGAGCGGGGGGAGGCGGCGCTGAGAGGAGGAGGAGGAGGAGGAGG 270  
DB 732 TTGG 791  
QY 271 GTGGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 323  
DB 792 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 844

RESULT 29  
CNS0060N/c

LOCUS 910 bp DNA linear GSS 03-JUN-1999  
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC #  
BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION AL065629  
VERSION AL065629.1 GI:4944698

KEYWORDS GSS.  
ORGANISM Drosophila melanogaster (fruit fly)

SOURCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 910)  
Genoscope.

REFERENCE Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

COMMENT Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs for further information  
please see <http://www.fruitfly.org> The BDGP Drosophila  
melanogaster BAC library was prepared by Kazutyo Oosawa and  
Aron Mammoser in Peter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPCI-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain Y2; cn bw sp, the same strain used for the BDGP s

P1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).  
Location/Qualifiers

1. .910

/organism="Drosophila melanogaster"  
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/clone="BACR14J21"  
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/note="end : T7"

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ORIGIN

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Best Local Similarity 15.6%; Pred. No. 0.042;  
Matches 48; Conservative 148; Mismatches 112; Indels 0; Gaps 0;

QY 16 CCGCAAGCGAAGGTGGGCGGCGGCTCTCGCGAGACAAAGCGGCGCTCTC 75  
DB 819 VSRASVSVSVSASASRSASVSSSSSAGSAVSAVMAASVMAVMSASVVA 760  
QY 76 TCTCAGAGGCGCCGAGGCTTCCAGAGAGAGTCTCTGAGGCGCGGAGGAGG 135  
DB 759 ARAAKASASVAVAVAVAVASAAVAVASVAVASVAVASVAVASVAVAS 700  
QY 136 CACGAGCTCCAGAGGCGCCGCGCGAGAGAGAGAGAGAGAGAGAGAGAG 195  
DB 699 SSSASASASASASASASVMSVMSVMSVMSVMSVMSVMSVMSVMSVMS 640  
QY 196 GAGCGGCGAGGCTTCTCAGAGGCGCGGCGGCGGCGGCGGCGGCGGCGG 255  
DB 639 SSSGSSVSCSSRCCGASASASASASGSSSSSSSSSSSSSSSSSSSSSS 580  
QY 256 GGTATAGAGAGCGGCGGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 315  
DB 579 SSVGCVSS 520  
QY 316 CCGCGCGC 323  
DB 519 CCGSCCC 512

RESULT 30  
B2046906/c

LOCUS 723 bp DNA linear GSS 09-OCT-2002  
DEFINITION Ik119g10.b1 B.oleracea002 Brassica oleracea genomic, genomic survey  
sequence.

ACCESSION B2046906  
VERSION B2046906.1 GI:23642870

KEYWORDS GSS.  
ORGANISM Brassica oleracea

SOURCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
1 (bases 1 to 723)  
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash  
W., Rabinowicz, P.D. and Wilson, R.K.  
Whole genome shotgun reads from Brassica oleracea  
unpublished

REFERENCE Contact: Richard K. Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: [submissions@wustl.edu](mailto:submissions@wustl.edu)  
Plate: Ik119 row: g column: 10  
Seq primer: -210bp forward  
Class: shotgun  
High quality sequence start: 38  
High quality sequence stop: 159.  
Location/Qualifiers

1. .723

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/clone="BACR14J21"  
/clone\_1b="RPCI-98"  
/note="end : T7"

BASE COUNT 202 a 63 c 112 g 198 t 335 others  
ORIGIN

Query Match 17.8%; Score 57.6; DB 29; Length 910;  
Best Local Similarity 15.6%; Pred. No. 0.042;  
Matches 48; Conservative 148; Mismatches 112; Indels 0; Gaps 0;

QY 16 CCGCAAGCGAAGGTGGGCGGCGGCTCTCGCGAGACAAAGCGGCGCTCTC 75  
DB 819 VSRASVSVSVSASASRSASVSSSSSAGSAVSAVMAASVMAVMSASVVA 760  
QY 76 TCTCAGAGGCGCCGAGGCTTCCAGAGAGAGTCTCTGAGGCGCGGAGGAGG 135  
DB 759 ARAAKASASVAVAVAVAVASAAVAVASVAVASVAVASVAVASVAVAS 700  
QY 136 CACGAGCTCCAGAGGCGCCGCGCGAGAGAGAGAGAGAGAGAGAGAGAG 195  
DB 699 SSSASASASASASASASVMSVMSVMSVMSVMSVMSVMSVMSVMSVMS 640  
QY 196 GAGCGGCGAGGCTTCTCAGAGGCGCGGCGGCGGCGGCGGCGGCGGCGG 255  
DB 639 SSSGSSVSCSSRCCGASASASASGSSSSSSSSSSSSSSSSSSSSSS 580  
QY 256 GGTATAGAGAGCGGCGGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 315  
DB 579 SSVGCVSS 520  
QY 316 CCGCGCGC 323  
DB 519 CCGSCCC 512

/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3712"  
/clone\_lib="B.oleracea02"  
/note="Vector: pOTw13; Whole genome shotgun library from  
flowering buds. DNA was purified from a crude nuclear  
prep using Brassica oleracea T01000D3 buds provided by  
Thomas Osborn at the University of Wisconsin. Genomic  
DNA was provided by Pablo Rabinowicz (CSHL) and the  
shotgun library prepared at Washington University Genome  
Sequencing Center."

BASE COUNT 64 a 360 c 211 g 79 t 9 others

Query Match 17.8%; Score 57.4; DB 28; Length 723;  
Best Local Similarity 48.6%; Pred. No. 0.046;  
Matches 157; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 1 GCGGCTGGGCTCAACCGCAAGAGTGGGCGGGGCTCGCGAGCAAA 60  
| | | | |  
DB 635 GGGCGGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 576  
| | | | |  
QY 61 GCGCGGCTGCTCTCTCTCAAGAGCGCCCGCGCGCGCGCGCGCGCG 120  
| | | | |  
DB 575 GCGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 516  
| | | | |  
QY 121 GGGGAGGAGAGGGGGGCAAGCGGCTTCCAGAGCGCGCGCGCGAGAA 180  
| | | | |  
DB 515 GGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 456  
| | | | |  
QY 181 GCGAGCGCGCTGACCGGAGCGGCGGCTTTCTCAAGAGCGCGCGCGCG 240  
| | | | |  
DB 455 GCGGCG 396  
| | | | |  
QY 241 GAGGAGCGAGAGCGGGTATTAAGAGCTGTGGCTTTGCGGCGCGCGAG 300  
| | | | |  
DB 395 GGGGCG 336  
| | | | |  
QY 301 GCG 323  
| | | | |  
DB 335 GGGGCGCTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 313  
| | | | |

RESULT 31  
LOCUS CNS010RY/776 bp DNA linear GSS 26-JUL-1999  
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC  
BACN04P24 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION AL093932  
VERSION AL093932.1 GI:5610963  
KEYWORDS GSS.  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 1776)  
Genoscope.  
REFERENCE  
AUTHORS Direct Submission  
TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT Determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
library (DrosBAC) was made by Alain Billand at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector  
pBel0BAC11.

FEATURES  
source Location/Qualifiers  
1..776

/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone\_lib="BACN04P24"  
/clone\_lib="DrosBAC"  
/plasmid="pBel0BAC11"  
/note="end : SP6"

BASE COUNT 110 a 439 c 135 g 0 t 92 others

Query Match 17.8%; Score 57.4; DB 29; Length 776;  
Best Local Similarity 38.6%; Pred. No. 0.046;  
Matches 124; Conservative 43; Mismatches 154; Indels 0; Gaps 0;

QY 1 GCGGCTGGGCTCAACCGCAAGAGTGGGCGGGGCTCGCGAGCAAA 60  
| | | | |  
DB 356 GGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 297  
| | | | |  
QY 61 GCGCGGCTGCTCTCTCTCAAGAGCGCCCGCGCGCGCGCGCGCGCG 120  
| | | | |  
DB 296 GGGGAGGAGAGGGGGGCAAGCGGCTTCCAGAGCGCGCGCGCGAGAA 237  
| | | | |  
QY 121 GGGGAGGAGAGGGGGGCAAGCGGCTTCCAGAGCGCGCGCGCGAGAA 180  
| | | | |  
DB 236 GGGGAGGAGAGGGGGGCAAGCGGCTTCCAGAGCGCGCGCGCGAGAA 177  
| | | | |  
QY 181 GCGAGCGCGCTGACCGGAGCGGCGGCTTTCTCAAGAGCGCGCGCGCG 240  
| | | | |  
DB 176 GGGGAGGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 117  
| | | | |  
QY 241 GAGGAGCGAGAGCGGGTATTAAGAGCTGTGGCTTTGCGGCGCGCGAG 300  
| | | | |  
DB 116 GCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 57  
| | | | |  
QY 301 GCG 321  
| | | | |  
DB 56 GGGGCGCTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 36  
| | | | |

RESULT 32  
LOCUS B0957113/1019 bp mRNA linear EST 21-ANG-2002  
DEFINITION AGENCOURT\_8779542 NIH\_MGC\_18 Homo sapiens cDNA clone IMAGE:6371648  
5' UTR mRNA sequence.

ACCESSION B0957113  
VERSION B0957113.1 GI:22372591  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1019)  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
TITLE Contact: Robert Strausberg, Ph. D.  
COMMENT Email: sgabs-remail.nih.gov  
Tissue Procurement: DCTD/DRP/Gazdar  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LHCW546 row: c column: 09  
High quality sequence start: 25  
High quality sequence stop: 300.  
Location/Qualifiers  
1..1019

FEATURES  
source Location/Qualifiers  
1..1019  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6371648"



BASE COUNT	ORIGIN	50 a	506 c	311 g	99 t	53 others
Query Match	17.8%	Score 57.4	DB 13	Length 1019		
Best Local Similarity	48.3%	Pred. No. 0.04%				
Matches 157	Conservative	0	Mismatches 166	Indels 2	Gaps 1	
Qy	1	GGCGCTGGAGTCAAGCCGCAAGAGATGCGGGCCGGGGTGGGCTTCGCGAGACAA	60			
Db	769	GGCGCCGGGGGGGGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	710			
Qy	61	GGCGCGGCGCTCTCTCTCAAGAGGAGCCCGACGCGCTGCGCAAGAGAAATCCTCGAGGCC	120			
Db	709	GGCGCGGCGCGCGCGAGCGCGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	650			
Qy	121	GGGCGAGGAAAGGGGCGACGGGCTTCCAGAGGCGCCCGCGCGCGACAGAAATTTGGCGAG	180			
Db	649	GGCGCGGAGGCGCGCGGGGGGGGGCGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCG	590			
Qy	181	GGGACGCGCGCGTGAAGCGGA--GGGGCGAGAGGGCTTTCTCAAGAGCGCGGGCGAGCGCGCG	238			
Db	589	GGGGGGGGGGGGGGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	530			
Qy	239	TGAGAGGGCGGAGAGCGGGGTATTAAGAACTTCGTGGGCTTCGCCGGCGAGCGCAGTTC	298			
Db	529	GGCGGGGGGGGCGGCGCGGG	470			
Qy	239	CCCGCGCGCCCCCGAGCCCCCGCGCC	323			
Db	469	GGGGCGCGCGCGCGGGCGCGCGCGCC	445			
RESULT 33						
LOCUS	BG844318	873 bp	mRNA	linear	EST 29-MAY-2001	
DEFINITION	1024005H12.x2 C. reinhardtii CC-1690, normalized, Lambda Zap II					
VERSION	Chlamydomonas reinhardtii cDNA, mRNA sequence.					
KEYWORDS	CG844318					
SOURCE	CG844318.1 GI:14225502					
ORGANISM	EST.					
REFERENCE	Chlamydomonas reinhardtii					
AUTHORS	Chlamydomonas reinhardtii					
TITLE	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;					
JOURNAL	Chlamydomonas reinhardtii					
COMMENT	Chlamydomonas reinhardtii					
	1 (bases 1 to 873)					
	Grossman,J.P., Davies,J., Federpiel,N., Harris,E., Lefebvre,P.,					
	McGermott,J.P., Silefow,C., Stern,D. and Surzycki,R.					
	Analyses of the Chlamydomonas reinhardtii Genome: A Model,					
	Unicellular System for Analyzing Gene Function and Regulation in					
	Vascular Plants; project phase 2					
	Unpublished					
	Contact: Charles Hauser					
	DCMB Box 91000					
	Duke University					
	Durham, NC 27708-1000					
	Tel: 919 613 8155					
	Fax: 919 613 8177					
	Email: chausser@duke.edu					
	Location/Qualifiers					
	1..873					
	/organism="Chlamydomonas reinhardtii"					
	/mol_type="mRNA"					

		/strains="CC-1690 wild type mt + 21gr"	
		/db_xref="taxon:1055"	
		/c1one_1lb="C. reinhardtii CC-1690, normalized, Lambda Zap II"	
		/note=Vector: pBluescript II SK <sup>+</sup> , Site 1: EcoRI; Site 2: XhoI; This library, constructed by John Davies and Jeffery McDermott, contains cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO <sub>2</sub> and HS medium bubbled with 5% CO <sub>2</sub> . PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. ZAP clones by superinfection with Exsist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."	
BASE COUNT	17 a	334 c	471 g 22 t 29 others
ORIGIN			
Query Match	17.7%;	Score 57.2;	DB 12; Length 873;
Best Local Similarity	50.5%;	Pred. No. 0.05;	
Matches 163;	Conservative 0;	Mismatches 159;	Indels 1; Gaps 1;
OY	1	GCGCGTGGGAGCAACGCCGAAGAGTGATCGGGCGGTGGCTCCGCAGACAATA	60
Db	398	GGGCGGCGGCGCCCGCGGGCGCCGGGCGGGGGGGCGGGGGGCGGCGCGCGCGC	457
OY	61	GCGCGGCGCTTCCTCTCAAGAGGCGCCAGCGCGCTCCAAAGAGAATCCTCGAGCGC	120
Db	458	GGGGGCGGCGCGCGCGCGGGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC	517
OY	121	GCGGAGGAAAGGGGGGACAGCGGCTTTCCAAGGCGCGCGCGCGCGAGAGATTGGCAG	180
Db	518	GCGGCGCGGGGGCGG	577
OY	181	GGCACGCGCGTGAAGCGGAGCGGGCGAGGCTTTCTCAGAAGTCCGGCGAAGCGCGCGCTG	240
Db	578	GCGGCGGG	636
OY	241	GAGGGGCGAGGACCGGGGATTAAAGAGCTCTGTGGCTTTGCCCGGGGACGCGGAGATTCCC	300
Db	637	CGCGGGCGCGCGCCCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	696
OY	301	CGCGCGCGCGCGAGCGCCCGCGCGC	323
Db	697	GCGCGGGCGCGGGGGCGGGGGCGCGC	719
RESULT 34			
LOCUS	AG136798	828 bp	DNA linear GSS 04-NOV-2001
DEFINITION	Pan troglodytes DNA, clone: PTB-150H19.R, genomic survey sequence.		
ACCESSION	AG136798		
VERSION	AG136798.1	GI:16666476	
KEYWORDS	GSS.		
SOURCE	Pan troglodytes (chimpanzee)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.		
REFERENCE	1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Tokoki, Y., Watanabe, H., and Sakaki, Y.		
TITLE	BAC end sequences of Library PTB		
JOURNAL	Unpublished		
REFERENCES	2 (bases 1 to 828) Direct Submission Submitted (02-AUG-2001) Aao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,		

## COMMENT

Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB. This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.

## PRIMERS

Sequencing: M13Rev  
Library Vector : PKS145  
R.Site 1 : SacI  
R.Site 2 : SacI

## FEATURES

Location/Qualifiers  
1 828  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-150H19.R"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 22 a 147 c 479 g 27 t 153 others  
ORIGIN

Query Match 17.6%; Score 57; DB 29; Length 828;  
Best Local Similarity 50.7%; Pred. No. 0.055;  
Matches 152; Conservative 0; Mismatches 147; Indels 1; Gaps 1;

23 GCGAAGTGCAGGCGCGGGGTGGGCTTCGCGGAGACAAAGCCGGGCTCTCTTCACG 82  
Db GNNNGGGGGGGGGCTGTGGGGGGCGCCCAAAAGAGGGGGGGGCGCCGGGG 494  
Qy GGGCCCCAGCGCTGCCAAGAGAGTCTTCGAGGCCCGGCGAGGAGGGGCGACGGGC 142  
Db GGGCGCGGGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 554  
Qy 143 TTCCAGAGGCGCGCGCGCGCGAGAGATTGGCCAGGGCGACGGCGCTGAGCGAGCGG 202  
Db GCGGGGGGGGGCGCGGGGGCGCGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGG 614  
Qy 203 GCAGGGCTTTCTCAGAGCGCGGGCGAGCGCGC-GCTGAGGGGGCGAGACCGGGTATTA 261  
Db 615 CCCGGGCGCGCGCGCGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 674  
Qy 262 AGAAGCGCTCGTGGCTTGGCCCGGGCGAGCGCGAGTTCCCGCGCGCGCGCGCGCG 321  
Db 675 CCGGGCGCGCGCGCGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 734

## RESULT 35

BO678466/c 971 bp mRNA linear EST 15-JUL-2002  
LOCUS AGENCOURT 8208927 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:5260268  
DEFINITION 5', mRNA sequence.

ACCESSION BO678466

VERSION BO678466.1 GI:21791145

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC http://mgi.nci.nih.gov/

1 (bases 1 to 971)  
National Institutes of Health, Mammalian Gene Collection (MGC)

AUTHORS Unpublished

TITLE Contact: Robert Strausberg, Ph.D.

JOURNAL Email: cgapbs-remail.nih.gov

COMMENT Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LNCM2419 row: b column: 13

## FEATURES

source

High quality sequence stop: 536.

Location/Qualifiers

1..971  
/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6260268"

/issue\_type="melanotic melanoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 112"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGCGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH MGC Library."

BASE COUNT 143 a 366 c 267 g 107 t 88 others  
ORIGIN

Query Match 17.6%; Score 56.8; DB 13; Length 971;  
Best Local Similarity 41.3%; Pred. No. 0.061;  
Matches 124; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

23 GCGAAGTGCAGGCGCGGGGTGGGCTTCGCGGAGACAAAGCCGGGCTCTCTTCACG 82  
Db GGGGGGGGGGGGGGCGGNNNGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 898  
Qy 957 GGGGGGGGGGGGGGCGGNNNGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 898  
Db 83 GGGCCCCAGCGCTGCCAAGAGAGTCTTCGAGGCCCGGCGAGGAGGGGCGACGGGC 142  
Qy 897 GGGGGNNNGGGNNNGGNNCGCGGGGNNCGGGGGNNNGGGGGGGGGGGGGGGGG 838  
Db 143 TTCCAGAGGCGCGCGCGCGCGAGAGATTGGCCAGGCGACGCGCTGAGCGAGCGG 202  
Qy 837 GNNCGCGCGGNNNNCCNNNNNGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 778  
Db 203 GCAGGGCTTTCTCAGAGCGCGGGCGAGCGCGCTGAGGGGGCGAGACCGGGTATTA 262  
Qy 777 GGCNCGCGGG 718  
Db 263 GAAGCTCGTGGCTTGGCCCGGGCGAGCGCGAGGTTCCCGCGCGCGCGCGCGCGCG 322  
Qy 717 GNNCCCCCGGGGGCGCGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 658

## RESULT 36

BU185501 1126 bp mRNA linear EST 04-SEP-2002  
LOCUS AGENCOURT 8108662 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6253571  
DEFINITION 5', mRNA sequence.

ACCESSION BU185501

VERSION BU185501.1 GI:22699485

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC http://mgi.nci.nih.gov/

1 (bases 1 to 1126)  
National Institutes of Health, Mammalian Gene Collection (MGC)

AUTHORS Unpublished

TITLE Contact: Robert Strausberg, Ph.D.

JOURNAL Email: cgapbs-remail.nih.gov

COMMENT Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LNCM2401 row: k column: 12

High quality sequence start: 70

FEATURES High quality sequence stop: 292.  
Location/Qualifiers  
Source 1. 1126  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6253571"  
/issue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1b="NIH\_MGC\_112"  
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

BASE COUNT 57 a 331 c 625 g 89 t 24 others

ORIGIN

Query Match 17.5%; Score 56.4; DB: 13; Length 1126;  
Best Local Similarity 48.8%; Pred. No. 0.073;  
Matches 144; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 28 GGTGCGGCGCGGCTGCGCGAGACAAAGCCCGCTCTCTCAAGAGCC 87  
DB 548 GGTGCGGCGCGGCTGCGCGAGACAAAGCCCGCTCTCTCAAGAGCC 607  
QY 88 CCAAGCGCTGCGCAAGAAATCTTCAGAGCCCGCGAGGAAAGCGCTTCCC 147  
DB 608 GCGGCG 667  
QY 148 AGGCG 207  
DB 668 GCGGCG 727  
QY 208 GCTTTTCAGAGACCGCGCGAGCGCGCGCTTGAAGCGCGAGACCGGCTTAAGAAC 267  
DB 728 GCGGCG 787  
QY 268 CTCGTGCGCTTTCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 322  
DB 788 GCGGCG 842

RESULT 37  
BO892481 1150 bp mRNA linear EST 16-AUG-2002  
LOCUS BO892481  
DEFINITION BO892481 8296668 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6249766  
5', mRNA sequence.  
ACCESSION BO892481  
VERSION BO892481.1 GI:22284495  
KEYWORDS EST  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1150)  
AUTHORS NIH-MGC. <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [gsr@frcmail.nih.gov](mailto:gsr@frcmail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LNCM2391 row: 1 column: 23  
High quality sequence start: 20

FEATURES High quality sequence stop: 171.  
Location/Qualifiers  
Source 1. 1150  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6249766"  
/issue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1b="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

BASE COUNT 39 a 550 c 358 g 70 t 133 others

ORIGIN

Query Match 17.5%; Score 56.4; DB: 13; Length 1150;  
Best Local Similarity 48.1%; Pred. No. 0.073;  
Matches 156; Conservative 0; Mismatches 166; Indels 2; Gaps 1;

QY 2 CGCTGCGGCTCAACCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 61  
DB 658 GCGGCG 599  
QY 62 GCGGCG 121  
DB 598 CCGGCG 539  
QY 122 GCGAGGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 179  
DB 538 GCGGCG 479  
QY 180 GCGGCG 239  
DB 478 GCGGCG 419  
QY 240 GGAAGGCGCGAGACCGGCTTAAGAACCTCTGAGCGCGCGCGCGCGCGCG 299  
DB 418 GCGGCG 359  
QY 300 CCGGCG 323  
DB 358 NCCCCCG 335

RESULT 38  
AG060267 810 bp DNA linear GSS 03-NOV-2001  
LOCUS AG060267  
DEFINITION Pan troglodytes DNA, clone: PTB-047L09.R, genomic survey sequence.  
ACCESSION AG060267  
VERSION AG060267.1 GI:16611499  
KEYWORDS GSS  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
REFERENCE 1  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
Toto, Y., Watanabe, H., and Sakaki, Y.  
TITLE BAC end sequences of library PTB  
JOURNAL Unpublished  
COMMENT 2 (bases 1 to 810)  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
Toto, Y., Watanabe, H., and Sakaki, Y.  
TITLE Direct Submissions  
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),  
1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan



was generated during the R&D process and may have higher chance of  
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## PRIMERS

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LIBRARY

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R.Site 2 : SacI

Location/Qualifiers

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